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(54) TIME: SBRUM BIOMARKERS IN LUNG CANCER

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For two-tener codes and other abbreviations, refer to the "Guid-ance Notes on Codes and Abbreviations" appearing at the begin-ning of each regular issue of the PCT Gazene.

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SERUM BIOMARKERS IN LUNG CANCER

BACKGROUND OF THE INVENTION

[0001] The present invention relates generally to the field of serum biomarkers in imp careinoma. More particularly, the invention relates to serum biomarkers that can listinguish hing cancer from normal.

[0002] Lung cancer is the leading cause of cancer death worldwide, resulting in 150,000 deaths per year in the United States. The mortality rate from lung cancer is greater than the combined mortality from breast, prostate and colorectal cancers. On the basis of morphology, lung cancer can be broadly classified into four main categories namely, adenocarcinoma, aquamous cell carcinoma, large cell undifferentiated carcinoma and small cell carcinoma. In Hong Kong from 1990 to 1996, the proportions for adenocarcinoma, aquamous cell carcinoma, large cell undifferentiated carcinoma and small cell carcinoma are 45.5%, 27.5%, 4.7% and 10.3% respectively. Both aquamous cell carcinoma and small cell carcinoma are strongly associated with a smoking history.

(0003) Adenocarcinoma, squamous cell carcinoma, and large cell undifferentiated carcinoma are usually referred as "non-small cell carcinoma." They are relatively chemo-resistant, and hence the mainstay of treatment is surgery. By contrast, small cell carcinoma has a higher propensity for distant metastases and is mainly treated by chemotherapy.

[0004] Biopsy can be used to diagnose lung cancer, but it is an invasive procedure and, therefore, less than desirable. Other diagnostic methods for lung cancer include ultrasound and computed tomography (CT) scan.

[0005] It would be highly desirable to have a blomarker or combination of biomarkers capable of distinguishing between hung cancer and normal cells. In addition, a simple test could aid in tracking treatment progress and even identify molecular targets for therapy. The literature on hung cancer diagnosis has not disclosed haretofore such a biomarker or combination of biomarkers, however.

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SUMMARY OF THE INVENTION

[0006] In accordance with the present invention, biomarkers and combinations of biomarkers are used to identify lung cancer. The method successfully distinguishes between lung cancer and normal states, and can be used to identify the particular type of lung cancer. In one embodiment, a method for qualifying lung carcinoma status in a subject (e.g., a patient) comprises analyzing a biological sample from the subject for one or more of the top 50 biomarkers as shown in Figure 2 or Figures 4A and 4B. Thus, to assess overall lung cancer risk versus normal, a biomarker is selected from the group consisting of

(A) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-165, IM-165, IM-157, IM-476, IM-468, IM-438, IM-547, IM-359, IM-378, IM-436, IM-465, IM-444, IM-168, IM-56, IM-50, IM-159, IM-156, IM-439, IM-167, IM-508, IM-514, IM-478, IM-473, IM-360, IM-154, IM-161, IM-514, IM-514, IM-478, IM-473, IM-360, IM-153, IM-150, IM-517, IM-514, IM-437, IM-548, IM-153, IM-161, IM-110, IM-51, IM-163, IM-437, IM-548, IM-153, IM-161, IM-161, IM-51, IM-163, IM-437, IM-548, IM-153, IM-163, IM-163, IM-548, IM-548, IM-5488, IM-54888, IM-54888, IM-54888, IM-54888, IM-54888, IM-54888, IM-54888, IM-54888, IM-54888,

(B) WM-61, WM-447, WM-448, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-62, WM-366, WM-473, WM-47, WM-384, WM-276, WM-428, WM-428, WM-384, WM-292, WM-431, WM-456, WM-20, WM-384, WM-367, WM-36, WM-36, WM-36, WM-36, WM-36, WM-36, WM-36, WM-389, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310, WM-360, WM-48, WM-38, WM-138, and WM-400, WM-48, WM-380, WM-480, WM-

[0007] wherein the biomarker is differentially present in samples of a subject with lung cancer and a so-called 'normal" subject that is free of lung cancer.

[0008] More preferably, one or more of the top 15 biomarkers as shown in Figure 2 or Figures 4A and 4B is used to qualify lung cancer status. Thus, for assessing overall lung cancer status versus normal, the protein is selected from the group consisting of

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IM-266, IM-637, IM-471, IM-510, IM-544, IM-474, IM-155, IM-471, IM-(A) IM-522, IM-273, IM-520, IM-519, IM-464, IM-507, IM-521, IM-148, 510, IM-544, IM-474, and IM-155, or B) WM-81, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, VM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70.

for overall lung cancer status versus normal, the biomarker is selected from the group Figure 2 or Figures 4A and 4B is used to qualify lung cancer status. In this instance, [0009] Still more preferably, one or more of the top 5 biomarkers as shown in

(A) IM-522, IM-273, IM-520, IM-519, and IM-454, or

(B) WM-61, WM-447, WM-446, WM-133, and WM-119.

[0010] In one embodiment, the method measures a plurality of biomarkers. The phrality of biomarkers can be measured simultaneously.

tatus in a subject (e.g., a patient), comprising (A) providing a spectrum generated by 0011] Biomarkers that, by themselves, are able to identify hung cancer include the ubjecting a biological sample from said subject to mass spectroscopic analysis that nchades profiling on a chemically-derivatized affinity surface, and (B) putting the Thus, for qualifying overall lung cancer status, the biomarker is selected from the, 0012] The present invention also provides a method for qualifying lung cancer selected from the top 50 biomarkers as shown in Figure 2 or Figures 4A and 4B. PM-446 and WM-447 protein biomarkers, and these are particularly preferred. pectrum through pattern-recognition analysis that is keyed to at least one peak group consisting of

M-268, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-436, IM-108, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-(i) IM-622, IM-273, IM-520, IM-519, IM-454, IM-507, IM-621, IM-148, 176, IM-446, IM-177, IM-440, IM-488, IM-438, IM-547, IM-359, IM-

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B) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-282, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-298, WM-343, WM-341, WM-339, WM-56, WM-66, WM-48, WM-38, WM-138, and WM-WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277,

(0013) For assessing the overall lung cancer status, the pattern-recognition analysis (A) IM-266 and IM-474, IM-266 and IM-38, IM-266 and IM-454, IM-265 may, for example, be paired to a pair of peaks selected from the group consisting of and IM-522, IM- 286 and IM-544, IM-268 and IM-471, IM-474 and IM-151, IM-474 and IM-156, IM-474 and IM-544, IM-474 and IM-38, IM-522 and IM-507, IM-522 and IM-158, and IM-522 and IM-440;

WM-447 and WM-473, WM-19 and WM-59, WM-19 and WM-473, WM-19 and WM-369, WM-61 and WM-154, WM-61 and WM-369, WM-118 (B) WM-447 and WM-59, WM-447 and WM-19, WM-447 and WM-118, and WM-59 and WM-282 and WM-127.

recognition analysis is keyed to a pair of peaks selected from the group consisting of (A) IM-266 and IM-474, IM-266 and IM-544, and IM-156 and IM-522; [6014] More preferably, for assessing overall hing cancer status, the pattern(B) WM-447 and WM-59, WM-447 and WM-19, and WM-19 and WM-59. cancer status may be keyed to a triplet of peaks selected from the group consisting of [0015] Alternatively, the pattern-recognition analysis for assessing overall lung (A) IM-266, IM-454 and IM-474; and IM-268, IM-474 and IM-544;

(B) WM-447, WM-19 and WM-473.

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[0016] In other embodiments, the pattern-recognition analysis may be keyed to a combination of more than three peaks, more particularly to a combination of 4, 5 or 6 peaks, where the combination is selected from among the combinations shown in Tables 1 and 2 herein.

[6017] In each case, the biomarker is differentially present in samples of a subject with hing cancer and a normal subject.

nanufacture in which one or more biomarkers according to the invention are bound to spectrun generated by mass spectroscopic analysis of a biological sample taken from embodiment, the algorithm comprises classification tree analysis that is keyed to data biomarkers shown in Figure 2 or Figures 4A and 4B, and (ii) instructions to detect the NCX and IMAC biochip. In addition, the kits may comprise one or more containers Atternatively, the kit may further comprise a second substrate adapted to engage the (1820) The present invention also provides software for qualifying hing carcinoma relating to at least one of the biomarkers. In yet another embodiment, the algorithm cancer, thereby to assess lung cancer status. Kits within the invention comprise, for include more than type of adsorbent, each present on a different substrate, e.g., on a malysis that is keyed to data relating to at least one of the biomarkers. In another vashing solution and/or instructions for making a washing solution. The kits may comprising the adsorbent may be designed to engage a probe interface and, hence, he subject, wherein said data relates to one or more biomarkers according to the unction as a probe in gas phase ion spectrometry, preferably mass spectrometry. 19018] The invention also contemplates a kit for detecting and diagnosing lung niomarker(s) retained by the adsorbent. An inventive hit may further comprise a vith biomarker samples, to be used as standard(s) for calibration. The substrate tams in a subject, comprising an algorithm for analyzing data extracted from a in adsorbent, optionally contacted with a matrix or energy absorbing molecule. nvention. In one embodiment, the algorithm carries out a pattern-recognition example, (i) an adsorbent attached to a substrate that retains one or more of the 0019] The method and kit according to the invention produce an article of nobe interface, on which the substrate comprising the adsorbent is mounted. biomarker(s) by contacting a sample with the adsorbent and detecting the

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comprises an artificial neural network analysis that is keyed to data relating to at least one of the biomarkers. [0021] In certain embodiments, the present invention provides methods and kits that use serum anyloid a protein or a fragment thereof to qualify lung cardinoma status in a subject. In one of these embodiments, the serum anyloid a biomarker has an apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Dattons. In another embodiment, the serum anyloid a biomarker has an apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, 7941, 8152, 8952, or 10851 Daltons. In yet another embodiment, the serum anyloid a biomarker has an apparent molecular weight of about 115 to 11.7 kD.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] Figures 1A-1D show all biomarkers identified with a Cu(II) IMAC3 ProteinChip® seray format.

[0023] Figure 2 shows the top 50 biomarkers identified with a Cu(II) IMAC3
ProteinChip@ array format.

[0024] Figures 3A-3O show all biomarkers identified with a WCX ProteinChip® stray format.

[0025] Figures 4A and 4B show the top 50 biomarkers identified with a WCX ProteinChip® array format.

[0026] Figure 5 shows fragments of serum amyloid A (SAA) that are biomarkers according to the present invention.

[0027] Figure 6 shows identification of SAA biomarkers with an anti-SAA antibody.

[0028] Figures 7-16 are spectra from WCX chips in which all of the top 15 WCX marker peaks are labeled, along with various other peaks from among the top 50 WCX peaks. Red shows spectra from hung cancer patients and gray shows normals. [0029] Figures 17-28 are spectra from DMAC chips in which all of the top 15 WCX marker peaks are labeled, along with various other peaks from among the top 50 IMAC peaks. Blue shows spectra from lung cancer patients and gray shows normals.

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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

iomarker is differentially present in samples taken from two groups of subjects if it is slevated or decreased level, as compared to subjects that do not have lung cancer. A .g., small cell carcinoma, as compared to a comparable sample taken from a subject polypeptide that is characterized by an apparent molecular weight, as determined by biomarker is differentially present between two sets of samples if the amount of the biomarker in one sample set differs in a statistically significant way (p < 0.01) from 10030) In accordance with the present invention, a series of biomarkers associated lifferentially present in a sample taken from a subject with one type of lung cancer, parcinoma, or differentially present at different stages of a type of lung cancer. A mass spectrometry, and that is present in samples from hung cancer subjects in an organic biomolecule, particularly a polypeptide or protein, which is differentially with lung cancer has been discovered. In the present context, a biomarker is an resent at an elevated level or a decreased level in samples of the first group as compared to samples of the second group. More particularly, a biomarker is a present in a sample taken from a subject having lung cancer as compared to a comparable sample taken from a normal subject. A blomarker also may be vith a different type of lung cancer, e.g., adenocarcinoma or squamous cell he amount of biomarker in the other sample set.

[0031] The blomarkers of the invention can be used to assess fung cancer steins in a subject. For example, they are capable of identifying lung cancer and successfully distinguishing it from normal subjects, thereby providing a way of diagnosing the presence or absence of lung cancer, including the presence or absence of a particular kind of lung cancer. In addition, the biomarkers are useful in assessing the risk of developing lung cancer, in staging of lung cancer and in assessing the effectiveness of treatment. Thus, "hung cancer status" in the context of the present invention includes, inter alla, the presence or absence of disease, tho risk of developing disease, the stage of the disease, and the effectiveness of treatment of disease. Based on this status, further procedures may be indicated, including additional diagnostic tests or therapeutic procedures or regimena, and radiation therapy.

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[0032] In some instances, a single biomarker is capable of identifying lung cancer with a sensitivity or specificity of at least 85%, whereas, in other instances, a combination or plurality of biomarkers is used to obtain a sensitivity or specificity of at least 85%. The biomarkers and combinations of biomarkers thus can be used to qualify lung cancer status in a subject or patient.

pio033] The biomarkers according to the invention are present in serum. The biological sample used according to the present invention, however, need not be a serum sample. Thus, a biological sample for qualifying lung cancer status may be a serum, plasma or blood sample, although serum samples are preferred.

10034] All of the biomarkers are characterized by molecular weight. A list of all the biomarkers obtained with the Cu(II) IMAC3 ProteinChip® array (Ciphergen Biosystems, Inc., Fremont, California, USA) is provided in Figures 1A-1D, and Figure 2 lists the top 50 biomarkers that distinguish between hung cancer and normal subjects that are identified by Cu(II) IMAC3 protocol described herein. Figures 3A-30 comprise a list of all the biomarkers obtained with the WCX2 ProteinChip® array, and Figures 4A and 4B comprises a ranking of the top 50 biomarkers that distinguish between (i) lung cancer and normal subjects, (ii) subjects with each of four types of lung cancer and normal subjects, and (iii) two types of lung cancer, e.g., adenocarcinoma versus squamous cell carcinoma, as identified by WCX2 protocol described herein.

10035] The top 50 biomarkers were determined by decision tree analysis using Biomarker PatternsTM software from Ciphergen Biosystems, Inc. Biomarkers other than those within the top 50 also are useful in distinguishing between subjects with img cancer and normal subjects and may, in particular, appear in decision trees with multiple nodes. In preferred embodiments, one or more of the top 15 biomarkers are used, and in even more preferred embodiments, one or more of the top 5 biomarkers are used, and in even more preferred embodiments, one or more of the top 5 biomarkers are used.

[0036] In each of Figures 1A-1D and 3A-3O, the number in the first column is the biomarker identifier. Thus, the first row in Figures 1A-1D relates to biomarker IM-1, the second row relates to biomarker IM-2, and so forth ("IM-" denoting biomarker identified with the IMAC chip). Similarly, the first row in Figures 3A-3O relates to

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biomarker WM-1 and the second row relates to biomarker WM-2 ("WM-" denoting biomarkers identified with the WCX2 chip). The number in the second column in Figures 1A-1D is the apparent molecular weight of the biomarker in daltons, as determined by mass spectrometry. In Figures 3A-3O, the apparent molecular weights for the biomarkers identified in the first column are reported in columns 3 through 11. The letter in the second column of Figures 1A-1D and the third column of Figures 3A-3O denotes the fraction in which the biomarker clutes in the protocol described herein; that is, biomarkers with an "A" clute in the first fraction, biomarkers with a "B" clute in the second fraction, and so forth. The fraction in which the biomarker clutes correlates with its pl, which biomarkers cluting at higher pl, having a higher pl, and biomarkers cluting at lower pl.

[0037] Presenting the mass and affinity characteristics of a given biomarker within the invention, as in this description, characterizes that biomarker so as allow one to obtain and measure it, in accordance with the teachings herein. If desired, any of the biomarkers can be sequenced, in order to obtain an amino acid sequence, but this is not required to practice the present invention.

such as trypsin and V8 protease, and the molecular weights of the digestion fragments can be used to search databases for sequences that match the molecular weights of the digestion fragments can be used to search databases for sequences that match the molecular weights of the digestion fragments generated by the various enzymes. Alternatively, if the biomarkers are not proteins included in known databases, degenerate probes can be made based on the N-terminal amino axid sequence of the biomarker, which the biomarker was initially detected. The positive clones can be identified, amplified, and their recombinant DNA sequences can be sequenced using techniques which are well known. Finally, protein biomarkers can be sequenced using protein ladder sequencing. Protein ladders can be generated by fragmenting the molecules and subjecting fragments to enzymatic digestion or other methods that sequentially remove a single amino axid from the end of the fragment. The ladder is then analyzed by mass spectrometry. The difference in masses of the ladder fragments identifies the amino axid removed from the end of the molecule.

[0039] Several biomarkers identified in accordance with the teachings of the present invention fit to serum amyloid A (SAA) or to a fragment of SAA. SAA is a well-known acute phase inflammatory marker. A number of the SAA biomarkers are identified in Figure 5 by both molecular mass and amino acid sequence. Most of those markers bound anti-SAA antibodies, as shown in Figure 6. The intact mass of SAA is 11.5 to 11.7 kD, and these biomarkers also have been identified by the present methodology. Fragments preferably have a molecular mass of at least about 200 Daltons, more preferably at least about 500 Daltons. In even more preferred embodiments, fragments have a molecular mass of at least about 800 Daltons, and most preferably at least about 1 Kilodalton.

fold40] In one embodiment, the fragments of SAA include a sequence of amino acids that is recognized by an epitope of an anti-SAA antibody. One way of identifying sulfable fragments for use in the present invention is to enzymatically digest SAA and test the resulting fragments for the ability to bind to an anti-SAA antibody. Fragments that bind anti-SAA antibody can be sequenced using techniques well-known in the art, although the sequence of the fragment is not needed to practice the invention with a fragment from the enzymatic digest that is identified as binding anti-SAA antibody, all that is required is to subject to the fragment to mass spectrometry to determine its mass.

[0041] The serum biomarkers according to the present invention were identified by comparing mass spectra of samples derived from sers from two groups of newly-diagnosed subjects, subjects with lung cancer and normal subjects. The subjects were diagnosed according to standard clinical criteria. Lung cancer subjects were histologically confirmed, and subjects without iung cancer were followed for at least 18 months following serum collection for any sign of hung cancer, to exclude subjects with asymptomatic lung cancer.

10042] Sera from each group of subjects was collected, and fractionated with Q Ceramic HyperDF ion exchange resin (Biosepra SA, France) into six fractions which eluted at different pH. Fraction A comprised the flow through plus pH 9 eluant, Fraction B comprised the pH 7 eluant, Fraction C comprised the pH 5 eluant, Fraction P comprised the pH 3 eluant, Fraction F

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comprised isopropyl alcohol/acetonitrile TFA cluant. Fractions A through F are

identified on Figures 7-28 as Fractions 1 through 6, respectively.

[0043] Bach fraction was diluted and applied to a ProteinChip® array, either a Court DA & 23 or W/727 chin array. Both of these chin arrays are moduced by

Cu(II) IMAC3 or WCX2 chip array. Both of these chip arrays are produced by

Ciphergen Biosystems, Inc. (Premont, CA).

[0044] The Cu(II) IMAC3 is an "immobilized metal affinity-capture" chip, with a nitrilotriscetic acid surface for high-capacity copper binding and subsequent affinity

capture of proteins with metal binding residues. Imidazole may be used in binding and washing solutions to moderate protein binding, including binding of non-specific proteins. Increasing the concentration of imidazole in the washing buffers reduces the

proteins. Increasing the concentration of imidazole in the washing buffers reduces the binding of the target proteins. It is produced by photopolymerizing 5-

methylacylamido-2-(N,N-biscarboxymethylamino)pentanoic acid (7.5 wt%) and N,N'-methylenebisacxylamide (0.4 wt%) using (-) riboflavin (0.02 wt%) as a photoinitiator. The monomer solution is deposited onto the chip substrate and

inradiated to photopolymerize. The chip then is activated with Cu(II). [10045] The WCX2 is a weak cation exchange array with a carboxylate surface to bind cationic proteins. The negatively charged carboxylate groups on the surface of the WCX2 chip interact with the positive charges exposed on the target proteins. The binding of the target proteins is reduced by increasing the concentration of salt or by increasing the pH of the weaking buffers.

[0046] Following application of the chuant fraction, the chips were incubated to allow the polypeptides in the cluant to bind to the sites on the chip by an affinity interaction. After incubation, each chip array was washed to remove polypeptides that bind non-specifically and buffer contaminants. That chip then was dried, and an energy absorbing molecule or matrix was applied to it, to facilitate desorption and ionization in a mass spectrometer.

10047] In the mass spectrometer, retained polypeptides were desorbed from the chip array by laser desorption and ionization in a ProteinChip® Reader, which is integrated with ProteinChip® Software and a personal computer to analyze proteins captured on chip arrays. The ion optic and laser optic technologies in the ProteinChip® Reader detects proteins ranging from small peptides of less than 1000 Da up to proteins of

300 kilodaltons or more, and calculates the mass based on time-of-flight. Ionized polypeptides were detected and their mass accurately determined by this Time-of-Flight (TOF) Mass Spectrometry.

Fugar (1 Or) Mass appetramenty.

[10048] The mass spectra obtained for each group were subjected to scatter plot analysis, to eliminate run-to-run variation. Protein clusters on the scatter plot that had the same pattern for both lung cancer and normal subjects, i.e., protein clusters that were either elevated in both groups of subjects or depressed in both groups of subjects or depressed in both groups of subjects or depressed in both groups of subjects, were eliminated as potential biomarkers. The remaining polypoptides were further analyzed for their ability to accurately identify subjects with hung cancer. Because the molecular weights were derived from scatter plot analysis, and because of limits on the ability of mass spectrometry to resolve molecular weights, the "absolute" molecular weight values given in Figures 1A-1D and 3A-3O actually represent approximate molecular weights.

[0049] The biomarkers of this invention are characterized by their mass-to-charge ratio as determined by mass spectrometry. The mass-to-charge ratio of each biomarker is provided in Figures 1A-1D and 3A-3O. For example, IM-1 in Figure 1A has a measured mass-to-charge ratio of 2011. The mass-to-charge ratios were determined from mass spectra generated on a Ciphorgen Biosystems, Inc. PBS II mass spectrometer. This instrument has a mass accuracy of about 4-0 15 percent. Additionally, the instrument has a mass resolution of about 400 to 1000 m/dm, where m is mass and dm is the mass spectral peak width at 0.5 peak height. The mass-to-charge ratio of the biomarkers was determined using Biomarker Wizard^{1M} software (Ciphergen Biosystems). Biomarker Wizard assigns a mass-to-charge ratio to a biomarker by clustering the mass-to-charge ratios of the same peaks from all the spectra analyzed, as determined by the PBSII, taking the maximum and minimum mass-to-charge-ratio in the cluster, and dividing by two. Accordingly, the masses provided reflect these specifications.

[0050] The biomarkers of this invention are further characterized by the shape of their spectral peak in time-of-flight mass spectrometry. Mass spectra showing peaks representing the biomarkers are presented in Figures 7-28. The biomarker identifier numbers from Figures 2 and 4A-4B, respectively, are shown next to the peak, along

with their rank, which is indicated in parentheses below the biomarker identifier

mber.

[0051] The biomarkers of this invention are further characterized by their binding properties on chromatographic surfaces. Most of the biomarkers bind to IMAC (Cu) or WCX adsorbents (e.g., the Ciphergen® IMAC (Cu) or WCX ProteinChip® arrays) after washing as described herein.

as the midpoint of a molecular-weight for a biomarker herein should be interpreted as the midpoint of a molecular-weight range. The accuracy of the mass spectrometer is +/-0.15%, and the actual molecular weight for a biomarker is therefore the value given, +/-0.15%, For example, the actual molecular weight for biomarker IM-273 is given, +/-0.15%, or between 11687 and 11722. Often, the range surrounding the "absolute" value given in the figure is no more than +/- 5 daltons (2006 to 2016 for IM-1), generally no more than +/- 3 daltons (2008 to 2014 for IM-1), and often as small as +/- 1 dalton (2010 to 2012 daltons for IM-1).

[0053] CART® (Salford Systems, San Diego, CA), a classification and regression tree software, was used to determine whether a potential biomarker had predictive value in assessing lung cancer. A software macro randomly selected a subset of 15% of the peaks from Figures 1A-1D or Figures 3A-3O. The peaks and peak heights from each sample were provided to the CART® software for analysis. The software performed an iterative analysis until a single decision tree was generated that was capable of distinguishing between cancerous and non-cancerous. Bach node in the resulting decision tree sorted based on the peak height of a single biomarker. A tree may contain any number of nodes, but generally contains from 1 to 6 nodes. From a practical standpoint in a commercial diagnostic test, a decision tree with fewer nodes is preferred. A total of 2000 decision trees, each based on a different 15% subset of the peaks from Figures 1A-1D or Figures 3A-3O, were generated.

[0054] The CART® software assigned a score to each biomarker in the subset, low. The CART® software also determined the sensitivity and specificity of each low. The CART® software also determined the sensitivity and specificity of each

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analysis. The data generated by the decision tree analysis was subjected to further analysis. The biomarkers were ranked based on their average scores, which were determined by adding up a biomarker's scores for each decision tree in which it appeared, and dividing by the total number of decision trees in which the biomarker appeared. Approximately 500 of the potential biomarkers showed up in at least one tree, and most of the biomarkers showed up in about 150 to 400 of the two thousand trees. The top 50 biomarkers for the IMAC and WCX chip arrays as determined by this method are shown in Figures 2 and 4A.4B, respectively.

[0056] All of the trees having sensitivities and specificities greater than 85% also were identified. All trees capable of distinguishing lung cancer from normal and having from 1 to 6 nodes that meet the 85/85 criterion are shown in Tables 1 and 2.

TABLE 1. Decision trees with IMAC Blomarkers.

2 Nodes			
474	151		
474	156		
522	507		2 trees
522	440		2 trees
3 Nodes	l l		•
266	454	474	
474	156	153	
474	40	156	
520	276	113	
620	265	401	
522	161	474	
522	478	153	
522	156	474	
4 Nodes			
148	521	508	251

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420 482 38

38. 203 474

5 Nodes

474 471

514

£	2	٥			
4 Nodes					
19	369	282	184		
61	48		3		
446	369	111	67		
446	466	58	120		
446	19	59	113		
446	282		47		
447	118	59	417		
447	118	29	473		
447	65	59	275		
447	19	59	282		
447	369	59	206		
447	19	59	253		
447	19	47	02		
5 Nodes					
61	369	128	184	. 281	
91	17	425	366	341	
133	139	363	216	273	
282	133	48	19	253	
369	310	19		384	
446	282	15	319	88	
447	19	71	473	31	
447	19	17	473	438	
447	47	31	365	59	
e Nodes					
369	366	192	471	19	439

TABLE 2. Decision Trees with WCX Biomarkers.

2 Nodes

1 Node

154 154 129 282

153 401

544

454 143

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combinations for distinguishing lung cancer subjects from normal subjects in 0057] Each of the biomarker combinations of Tables 1 and 2 are preferred accordance with the present invention.

times the biomarker occurred in a trees that met the criterion, as well as the ranking of entenion were identified. For these biomarkers, Tables 3 and 4 provide the number of 0058] All biomarkers that appeared in at least two of the trees that met the 85/85 that biomarker on the top 50 lists of Figures 2 and 4A-4B.

TABLE 3. Correlation of IMAC biomarker decision tree frequencles and

Peak	# times	Renk
266	6	6
522	8	-
474	4	14
520	2	3
148	1	8
273	-	2

TABLE 4. Correlation of WCX biomarker decision tree frequencies and

Peak	# times	Rank	
447	11	2	
19	10	1	
446	7	3	
282	4	9	
369	2	8	
133	2	4	

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473. Other repeating pairs and trios of biomarkers can be seen in Tables 3 and 4, and occurred among the top 50 ranked biomarkers, and typically had a top 10 ranking. In and WM-19, WM-19 and WM-59, IM-266 and IM-474, IM-266 and IM-38, IM-266 addition, certain pairs of biomarkers reappear, e.g., WM 447 and WM-59, WM-447 Diomarkers, such as IM-266, IM-266 and IM-38, and WM-447, WM-19 and WM-0059] Biomarkers that occurred frequently in the highly discriminatory trees nd IM-454, IM-522 and IM-266. There also are repeats among triplets of are preferred.

articular, a biomarker or combination of biomarkers can be used to distinguish lung 0060] Biomarkers and combinations of biomarkers identified in accordance with cancer patients from normal patients with a high degree of specificity or sensitivity, the present description may be used to qualify lung cancer status in a subject. In i.e., greater than at least 85%, preferably greater than at least 90%, and more preferably greater than 95%.

example, mass spectrometry. Other detection paradigms that can be employed to this end include optical methods, electrochemical methods (voltametry and amperometry techniques), atomic force microscopy, and radio frequency methods, e.g., multipolar resonance spectroscopy. Illustrative of optical methods, in addition to microscopy, spectrometry, which refers to the use of a gas phase ion spectrometer to detect gas detecting the biomarker bound to the adsorbent by gas phase ion spectrometry, for refractive index (e.g., surface plasmon resonance, ellipsometry, a resonant mirror biomarkens for diagnosis of lung cancer status entails contacting a sample from a chemiluminescence, absorbance, reflectance, transmittance, and birefringence or subject with a substrate, e.g., a SELDI probe, having an adsorbent thereon, under conditions that allow binding between the biomarker and the adsorbent, and then [0062] In one aspect, the markers of this invention are detect by gas phase ion both confocal and non-confocal, are detection of fluorescence, luminescence, (0061) According to one aspect of the invention, therefore, the detection of method, a grating coupler waveguide method or interferometry).

phase ions. A gas phase ion spectrometer is an apparatus that detects gas phase ions. Gas phase ion spectrometers include an ion source that supplies gas phase ions. Gas PCT/US2003/037090

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phase ion spectrometers include, for example, mass spectrometers, ion mobility spectrometers, and total ion current measuring devices.

pectrometers generally include an ion source and a mass analyzer: Examples of mass parameter which can be translated into mass-to-charge ratios of gas phase ions. Mass Laser desorption mass spectrometer" refers to a mass spectrometer which uses laser (0063) "Mass spectrometer" refers to a gas phase ion spectrometer that measures a spectrometers are time-of-flight, magnetic sector, quadrupole filter, ion trap, ion spectrometry" refers to the use of a mass spectrometer to detect gas phase ions. cyclotron resonance, electrostatic sector analyzer and hybrids of these. "Mass is a means to desorb, volatilize, and ionize an analyte.

interface that positionally engages a probe in an interrogatable relationship to a source provides gas phase ions. In one embodiment, the ion source provides ions through a 0065) "Ion source" refers to a sub-assembly of a gas phase ion spectrometer that communication at atmospheric or subatmospheric pressure with a detector of a gas comprises means for measuring a parameter which can be translated into mass-toof ionizing energy (e.g., a laser desorption/ionization source) and in concurrent charge ratios of gas phase ions. In a time-of flight mass spectrometer the mass desorption/ionization process. Such embodiments generally comprise a probe [0064] "Mass analyzer" refers to a sub-assembly of a mass spectrometer that malyzer comprises an ion optic assembly, a flight tube and an ion detector. phase ion spectrometer.

mergy delivered per unit area of interrogated image. Typically, a sample is placed on (used in plasma desorption); and (4) primary ions generating secondary ions (used in combardment); (3) high energy particles generated via beta decay of radionucleides phase analytes is a laser (used in laser desorption/ionization), in particular, nitrogen secondary ion mass spectrometry). The preferred form of ionizing energy for solid lasons, Nd-Yag lasons and other pulsed lason sources. "Fluence" refers to the lason he surface of a probe, the probe is engaged with the probe interface and the probe (0066) Forms of ionizing energy for desorbing/ionizing an analyte from a solid phase include, for example: (1) laser energy; (2) fast atoms (used in fast atom

surface is struck with the ionizing energy. The energy desorbs analyte molecules

from the surface into the gas phase and ionizes them

electrons which ionize gas phase neutrals; (2) strong electric field to induce ionization combination of ionization particles or electric fields with neutral chemicals to induce from gas phase, solid phase, or liquid phase neutrals; and (3) a source that applies a [0067] Ottier forms of ionizing energy for analytes include, for example: (1) chemical ionization of solid phase, gas phase, and liquid phase neutrals.

includes a solid substrate, either flexible or rigid, that has a sample-presenting surface, [0068] A preferred mass spectrometric technique for use in the invention is Surface the surface of a probe that presents the analyte (here, one or more of the biomarkers) interface and to present an analyte to ionizing energy for ionization and introduction U.S. patents No. 5,719,060 and No. 6,225,047, both to Hutchens and Yip, in which Enhanced Laser Desorption and Ionization (SBLDI), as described, for example, in into a gas phase ion spectrometer, such as a mass spectrometer. A probe typically molecules. In this context, "probe" refers to a device adapted to engage a probe to the energy source plays an active role in description/ionization of analyte on which an analyte is presented to the source of ionizing energy.

moiety that is capable of binding a capture reagent, $\epsilon_{\mathcal{S}}$, through a reaction forming a ("SELDI probe"). A "chemically selective surface" is one to which is bound either "SBAC," involves the use of probes comprised of a chemically selective surface the adsorbent, also called a "binding moiety" or "capture reagent," or a reactive [0069] One version of SELDI, called Surface-Enhanced Affinity Capture" or covalent or coordinate covalent bond.

moieties to covalently bind polypeptide capture reagents such as antibodies or cellular [0070] The phrase "reactive moiety" here denotes a chemical moiety that is capable noiety is bound. An "adsorbent" or "capture reagent" can be any material capable of receptors. Nitriloacetic acid and iminodiacetic acid are useful reactive moieties that uistidine containing peptides. A 'Yeactive surface'' is a surface to which a reactive function as chelating agents to bind metal ions that interact non-covalently with of binding a capture reagent. Epoxide and carbodiimidizole are useful reactive

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wids. A biospecific adsorbent typically has higher specificity for a target analyte than nacromolecular structure such as a multiprotein complex, a biological membrane or a ricus. Illustrative biospecifio adsorbents are autibodies, receptor proteins, and nucleic biomolecule, e.g., a nuclcotide, a mucleic acid molecule, an amino acid, a polypeptide, 0071] One type of adsorbent is a "chromatographic adsorbent," which is a material ypically used in chromatography. Chromatographic adsorbents include, for example, interaction adsorbents, hydrophilic interaction adsorbents, dyes, simple biomolecules on exchange materials, metal chelators, immobilized metal chelates, hydrophobic ipoprotein, a glycolipid). In certain instances the biospecific adsorbent can be a polyeaccharide, a lipid, a steroid or a conjugate of these (e.g., a glycoprotein, a according to the invention, are described in U.S. patent No. 6,225,047, supra. binding a biomarker of the invention. Suitable adsorbents for use in SELDI, e.g., nucleotides, amino acids, simple sugars and fatty acids), mixed mode adsorbents (a.g., hydrophobic attraction/electrostatic repulsion adsorbents). Biospecific adsorbent" is another category, for adsorbents that contain a chromatographic adsorbent.

and ionization of analyte molecules in contact therewith. The BAM category includes (19073) Another version of SBLDI, called Surface-Enhanced Photolabile Attachment bsorbing molecules" (EAM) denotes molecules that are capable of absorbing energy example, by U.S. 5,719,060 and U.S. 60/351,971 (Kinggawa), filed January 25, 2002. molecules used in MALDI, frequently referred to as "matrix," and is exemplified by (0072) Another version of SELDI is Surface-Enhanced Neat Desorption (SEND), iom a laser desorption ionization source and, thereafter, contributing to desorption breaking a photolabile bond in the moiety after exposure to light, e.g., to laser light. serivatives. The category also includes EAMs used in SELDI, as enumerated, for and Release (SBPAR), involves the use of probes having moieties attached to the which involves the use of probes comprising energy absorbing molecules that are surface that can coyalently bind an analyte, and then release the analyte through cimamic acid derivatives, sinapinic acid (SPA), cyano-hydroxy-cimamic acid (CHCA) and dihydroxybenzoic acid, ferulic scid, and hydroxyaceto-phenone chemically bound to the probe surface ("SEND probe"). The phrase "Energy

For instance, see U.S. 5,719,060. SEPAR and other forms of SELDI are readily adapted to detecting a biomarker or biomarker profile, pursuant to the present

or modify adsorption of an analyte to an adsorbent surface and/or to remove unbound naterials from the surface. The clution characteristics of a wash solution can depend phrase "wash solution" refers to an agent, typically a solution, which is used to affect or example, on pH, ionic strength, hydrophobicity, degree of chaotropism, detergent [0074] The detection of the biomarkers according to the invention can be enhanced by using certain selectivity conditions, e.g., adsorbents or washing solutions. The trength, and temperature.

a biochip comprises a plurality of addressable locations, each of which has the capture surface, to which a capture reagent (adsorbent) is attached. Frequently, the surface of means of a "biochip," a term that denotes a solid substrate, having a generally planar spectrometry. Alternatively, a biochip of the invention can be mounted onto another (6075) Pursuant to one aspect of the present invention, a sample is analyzed by reagent bound there. A biochip can be adapted to engage a probe interface and, hence, function as a probe in gas phase ion spectrometry preferably mass substrate to form a probe that can be inserted into the spectrometer.

biochips are those described in U.S. patents No. 6,225,047, supra, and No. 6,329,209 Wagner et al.), and in PCT publications WO 99/51773 (Kuimelis and Wagner) and accordance with the present invention, from commercial sources such as Ciphergen Biosystems (Fremont, CA), Perkin Bimer (Packard BioScience Company (Meriden СТ), Zyomyx (Науward, СА), and Phylos (Lexington, MA). Exemplary of these 0076 A variety of biochips is available for the capture of biomarkers, in WO 00/56934 (Englert et al.).

addressable locations, chromatographic or biospecific adsorbents. The surface of the surfaces, presented on an aluminum substrate in strip form, to which are attached, at [0077] More specifically, biochips produced by Ciphergen Biosystems have trip is coated with silicon dioxide.

WCX-2, and DAAC-3, which include a functionalized, cross-linked polymer in the [0078] Illustrative of Ciphergen ProteinChip@ arrays are biochips H4, SAX-2,

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functionalities that adsorb transition metal ions, such as Cu++ and Ni++, by chelation. coordinate covalent bonding. Thus, Ciphergen's IMAC ProteinChip@ arrays are sold with reactive moieties that become adsorbent upon the addition by the user of a metal attached through a silane to the surface of the biochip. The H4 blochip has isopropyl ammonium functionalities for anion exchange. The WCX-2 biochip has carboxylate form of a hydrogel, physically attached to the surface of the biochip or covalently functionalities for cation exchange. The IMAC-3 biochip has nitriloacetic acid These immobilized metal ions, in turn, allow for adsorption of biomarkers by functionalities for hydrophobic binding. The SAX-2 biochip has quaternary

is contacted with the sample, containing serum, for a period of time sufficient to allow [0079] In keeping with the above-described principles, a substrate with an adsorbent the biological sample. For example, a sample may be applied to both a WCX and an MAC chip. This technique can allow for even more definitive assessment of cancer material. Any suitable washing solutions can be used; preferably, aqueous solutions nvention, more than one type of substrate with adsorbent thereon is contacted with biomarker that may be present to bind to the adsorbent. In one embodiment of the status. After the incubation period, the substrate is washed to remove unbound are employed. 0080) An energy absorbing molecule then is applied to the substrate with the bound siomarkers from the substrate. Exemplary energy absorbing molecules include, as noted above, cinnamic acid derivatives, sinapinic acid and dihydroxybenzoic acid. energy from an energy source such as a laser, thereby assisting in desorption of niomarkers. As noted, an energy absorbing molecule is a molecule that absorbs Preferably sinapinic acid is used.

spectrometer such as a time-of-flight mass spectrometer. The biomarkers are ionized by an ionization source such as a laser, the generated ions are collected by an ion optic assembly, and then a mass analyzer dispenses and analyzes the passing ions. The detector then translates information of the detected ions into mass-to-charge 0081] The biomarkers bound to the substrates are detected in a gas phase ion

ignal and the determined molecular mass for each biomarker detected. Data analysis cleaner image and enabling biomarkers with nearly identical molecular weights to be he data to indicate the number of markers detected, and optionally the strength of the ratios. Detection of a biomarker typically will involve detection of signal intensity. [0082] Data generated by desorption and detection of biomarkers can be analyzed reference. The reference can be background noise generated by the instrument and display. The standard spectrum can be displayed, but in one useful format only the an include steps of determining signal strength of a biomarker and removing data conveniently highlighting unique biomarkers and biomarkers that are up- or downdeviating from a predetermined statistical distribution. For example, the observed peak beight and mass information are retained from the spectrum view, yielding a with the use of a programmable digital computer. The computer program analyzes chemicals such as the energy absorbing molecule which is set as zero in the scale. seaks can be normalized, by calculating the height of each peak relative to some [0083] The computer can transform the resulting data into various formats for more easily seen. In another useful format, two or more spectra are compared, Thus, both the quantity and mass of the biomarker can be determined.

0084] Software used to analyze the data can include code that applies an algorithm combination of biomarker peaks is present that indicates lung cancer status. Analysis of the data may be "keyed" to a variety of parameters that are obtained either directly or indirectly from the mass spectrometric analysis of the sample. These parameters to the analysis of the signal to determine whether the signal represents a peak in a height of one or more peaks, the log of the height of one or more peaks, and other include, but are not limited to, the presence or absence of one or more peaks, the ignal that corresponds to a biomarker according to the present invention. The classification tree or ANN analysis, to determine whether a biomarker peak or software also can subject the data regarding observed biomarker peaks to rithmetic manipulations of peak height data.

egulated between samples. Using any of these formats, one can readily determine

whether a particular biomarker is present in a sample.

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diagnosis of lung cancer status, which kits are used to detect biomarkers according to to invention. The kits screen for the presence of biomarkers and combinations of biomarkers that are differentially present in samples from normal subjects and 0085] In another aspect, the present invendon provides kits for aiding in the ubjects with hing cancer.

he biomarker using gas phase ion spectrometry, e.g., mass spectrometry. The kil may comprising an adsorbent thereon, and a second substrate onto which the first substrate s positioned to form a probe, which can be inserted into a gas phase ion spectrometer, which the combination of the adsorbent and the washing solution allows detection of (1987) In another embodiment, a kit of the invention may include a first substrate, .g., a mass spectrometer. In another embodiment, an inventive kit may comprise a invention, and a washing solution or instructions for making a washing solution, in thereon, wherein the adsorbent is suitable for binding a biomarker according to the 0086] In one embodiment, the kit comprises a substrate having an adsorbent nclude more than type of adsorbent, each present on a different substrate. ingle substrate that can be inserted into the spectrometer.

robe. In yet another embodiment the kit can comprise one or more containers with 0088] In a further embodiment, such a kit can comprise instructions for suitable nstructions may inform a consumer how to collect the sample or how to wash the perational parameters in the form of a label or separate insert. For example, the niomarker samples, to be used as standard(s) for calibration.

niomarkers are ionized by an ionization source such as a laser. The generated ions are 0089) In a preferred embodiment, the detection of biomarkers for diagnosis of lung strike the detector generate an electric potential that is digitized by a high speed timecollected by an ion optic assembly and accelerated toward an ion detector. Ions that cancer in a subject entails contacting a sample from a subject or patient, preferably a crum sample, with a substrate having an adsorbent thereon under conditions that Surface Enhanced Laser Description/Ionization (SELDI) mass spectrometry. The biomarker bound to the adsorbent by gas phase ion spectrometry, preferably by allow binding between the biomarker and the adsorbent, and then detecting the array reconding device that digitally captures the analog signal. Ciphergen's

epresent the signal from a single pulse of ionizing energy against a sample, but rather his. The ADC integrates detector output at regularly spaced time intervals into time-Ciphergen's ProteinChip@ software, data processing typically includes TOF-to-M/Z ransformation, baseline subtraction, high frequency noise filtering. Thus, both the ProteinChip® system employs an analog-to-digital converter (ADC) to accomplish Furthermore, the time-of-flight spectrum ultimately analyzed typically does not Jynamic range. This time-of-flight data is then subject to data processing. In dependent bins. The time intervals typically are one to four nanoseconds long. the sum of signals from a number of pulses. This reduces noise and increases quantity and mass of the biomarker can be determined.

imitar selectivity conditions that were used to discover the biomarkers are used in the 0090] The detection of the biomarkers can be enhanced by using certain selectivity conditions, e.g., adsorbents or washing solutions. In one embodiment, the same or nothod of detecting the biomarker in the sample. For example, immobilized metal effinity capture chips such as the Cu(II) IMAC3 and weak cationic exchange chips mch as the WCX2 chips are preferred as the adsorbents for biomarker detection. However, other adsorbents can be used, as long as they have the binding characteristics suitable for binding the biomarkers.

data include, but are not limited to, artificial neural network, support vector machines, plurality of samples assigned a negative diagnosis. The methods used to analyze the set that includes members of the different classes that are meant to be classified, for analysis. These methods are described, for example, in WO 01/31579, May 3, 2001 classification phase. In the learning phase, a learning algorithm is applied to a data riplets, and higher combinations of biomarkers according to the invention. These genetic algorithm and self-organizing maps and classification and regression tree 0091] More particularly, armed with the information regarding the biomarkers dentified herein, various methods can be used to recognize patterns of doublets, nethods take raw data regarding which peaks are present and their intensity and example, data from a plurality of samples diagnosed as cancer and data from a provide a differential diagnosis of lung cancer versus normal for a sample. 0092] Thus, the process can be divided into the learning phase and the

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(Bamhill et al.); WO 02/06829, January 24, 2002 (Hitt et al.) and WO 02/42733, May 30, 2002 (Paulse et al.). The learning algorithm produces a classifying algorithm. The classifier is keyed to elements of the data, such as particular markers and particular intensities of markers, usually in combination, that can classify an unknown sample into one of the two classes. The classifier is ultimately used for diagnostic testing.

[0093] Software, both freeware and proprietary software, is readily available to analyze such patterns in data, and to devise additional patterns with any predetermined criteria for success. Those biomarkers which by themselves are predictive of a differential diagnosis of lung cancer versus normal do not require pattern recognition software to analyze the data.

[0094] The following examples are offered by way of illustration, and are not imiting.

Example I. Fractionation of serum

3uffers:

- 1. U9 (9M urea, 2% CHAPS, 50mM Tris-HCl pH9)
- 2. U1 (1M urea, 0.22% CHAPS, 60mM Tris-HCI pH9)
- 3. wash buffer 1:50mM Tris-HCl with 0.1% n-octyl I-D-Glucopyrenoside (OGP) pH9
- 4. wash buffer 2: 100mM sodium phosphate with 0.1% OGP pH7
- 5. wash buffer 3: 100mM sodium acetate with 0.1% OGP pH5
- 8. wash buffer 4: 100mM sodium acatate with 0.1% OGP pH4
- 7. wash buffer 5: 50mM sodium citrate with 0.1% OGP pH3
- 8. wash buffer 6: 33,3% isopropanol / 16.7% acetonitrile / 0.1% trifluoroacetic acid in water.

[0095] Thirty microliters of U9 buffer were added to 20µL of serum in a tube and were mixed at 4°C for 20 minutes. Ion exchange resin (Q Ceramio HyperDF ion exchange resin, Biosepra SA, France) was washed 3 times with 5 bed volumes of 50mM Tris-HCl pH9 and stored in 50% suspension. To each well of a 96-well filter where 106. well Sinem Rarren filter where I animative rock-well Silter alone or 106.

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Nalge Nunc International, USA), 125 µL of ion exchange resin (50% suspension) was added on a Biomek 2000 Automation Workstation (Beckman Coulter, Pullerton, CA), washed 3 times with 150µL UI buffer, and vacuum dried. Urea-treated serum was transferred to each well of ion exchange resin. The serum tube was rinsed with 50µL of UI buffer, which was also transferred to the corresponding well in filter plate. The filter plate was mixed on a platform shaker at 4°C for 30 minutes. Flow-through fraction was collected in a 96-well plate by vacuum suction (Fraction 1). Then, 100µL of wash buffer 1 was added to each well of filter plate and mixed for 10 minutes at room temperature. Bluant was collected into the same 96-well plate (Fraction 1). Resins in the filter plate were subsequently washed two times each with 100µL wash buffers 2, 3, 4, 5 and 6. Each eluant (total volume of 200µL) was collected in a 96-well plate (Fractions 2,3,4,5 and 6).

Example 2. SELDI analysis of fractionated serum

10096] ProteinChip@ Arrays were set up in 96-well bioprocessors. Buffer delivery and sample incubation were performed on a Biomek 2000 Automation Workstation. Bach serum fraction was analyzed on IMAC3 (loaded with copper) and WCX2 ProteinChip@ Arrays in duplicates. IMAC3 copper and WCX2 arrays (Ciphergen Biosystems Inc, Premont, CA) were equilibrated two times with 150µL of binding buffer (100mM sodium phosphate + 0.5M NaCl pH7 for IMAC3, 100mM sodium acctate pH4 for WCX2). Each serum fraction was diluted in the corresponding binding buffer (1/5 dilution for IMAC3 and 1/10 dilution for WCX2) and 100µL was applied to each ProteinChip@ array. Incubation was performed on a platform shaker at room temperature for 30 minutes. Each array was washed three times with 150µL of corresponding binding buffer and rinsed two times with water. ProteinChip@ arrays were air-dried. Sinapinic acid matrix (prepared in 50% acconititie, 0.5% trifluoroacetic acid) was applied to each array. ProteinChip@ arrays were read on a ProteinChip@ PBSII Reader (Ciphergen Biosystems Inc.) A total of 253 laser shots were averaged for each array.

[0097] All publications and patent documents cited in this application are accorporated by reference in their entirety for all purposes to the same extent as if

each individual publication or patent document were so individually denoted. By their citation of various references in this document Applicants do not admit that any particular reference is "prior art" to their invention.

What we claim is:

 A method for qualifying lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a diagnostic level of a protein selected from either a first group consisting of

(i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-488, IM-438, IM-547, IM-359, IM-436, IM-136, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-478, IM-565, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-478, IM-546, IM-153, IM-163, IM-163, IM-546, IM-153, IM-268,

or from a second group consisting of

(ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-387, WM-430, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-66, WM-48, WM-38, WM-138, and WM-310,

wherein the biomarker is differentially present in samples of a subject with lung cancer and a normal subject that is free of lung cancer.

- The method according to claim 1, wherein the protein is selected from either a first group consisting of
- (j) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-711, IM-510, IM-544, IM-474, and IM-155,

or from a second group consisting of

- (ii) WM-61, WM 447, WM-146, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, and WM-70.
- The method according to claim 1, wherein the protein is selected from either a first group consisting of

 (j) IM-522, IM-273, IM-520, IM-519, and IM-454,
 or from a second group consisting

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- (ii) WM-61, WM-447, WM-446, WM-133, and WM-119.
- The method according to claim 1, which uses a single biomarker selected from the group consisting of the WM-446 and WM-447.
- A method for qualifying lung carcinoma risk in a subject, comprising (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- recognition analysis that is keyed to at least one peak selected from either a first group (B) extracting data from the spectrum and subjecting the data to patternconsisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

- WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, 296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, (ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, and WM-310.
- analysis is keyed to a pair of peaks selected either from a first group consisting of The method according to claim 5, wherein the pattern-recognition
- (i) IM-266 and IM-474, IM-266 and IM-38, IM-266 and IM-454, IM-266 and IM-522, IM-266 and IM-544, IM-266 and IM-471, IM-474 and IM-151, IM-474 and IM-156, IM-474 and IM-544, IM-474 and IM-38, IM-522 and IM-507, IM-522 and IM-156, and IM-522 and IM-440;

or from a second group consisting of

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WM-369, WM-61 and WM-154, WM-61 and WM-369, WM-118 and WM-59 and WM-447 and WM-473, WM-19 and WM-59, WM-19 and WM-473, WM-19 and (ii) WIM-447 and WIM-59, WIM-447 and WIM-19, WIM-447 and WIM-118, WM-282 and WM-127.

- 7. The method according to claim 5, wherein the pattern-recognition analysis is keyed to a pair of peaks selected from either a first group consisting of
- (i) IM-266 and IM-474, IM-266 and IM-544, and IM-156 and IM-522;
 - or from a second group consisting of
- (ii) WM-447 and WM-59, WM-447 and WM-19, and WM-19 and WM-59.
- The method according to claim 5, wherein the pattern-recognition analysis is keyed to a triplet of peaks selected from
- (i) IM-266, IM-454 and IM-474; and IM-266, IM-474 and IM-544;
- (ii) WM-447, WM-19 and WM-473.

or wherein the analysis is keyed to

- (A) an adsorbent attached to a substrate that retains one or more of the A kit for detecting and diagnosing hung carcinoma, comprising biomarkers selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-174, IM-155, IM-157, IM-176, IM-445, LK-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, M-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-56, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, (ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, 296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310, and

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- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- A hit according to claim 9, fluther comprising a washing solution or instructions for making a washing solution.
- comprises either (i) functionalities that adsorb transition metal ions by chelation or (ii) A kit according to claim 9, wherein the substrate is a SELDI probe that unctionalities that allow for cation exchange.
- 310, WM-292, WM-120, WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, 70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, WM-340, WM-48, WM-389, WM-450, WM-47, WM-343, WM-17, WM-583, WM-WM-473, WM-369, WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WMcomprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-A method for qualifying lung adenocarcinoma status in a subject, 307, WM-278, WM-342, and WM-429.
- The method according to claim 12, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292,
- The method according to claim 12, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290.
 - A method for qualifying status of hing adenocarcinoms in a subject,
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- recognition analysis that is keyed to at least one peak selected from either a first group WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, WM-340, WM-48, WMconsisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, WM-120, (B) extracting data from the spectrum and subjecting the data to pattern-

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WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WM-307, WM-278, WM-889, WM-450, WM-47, WM-343, WM-17, WM-583, WM-70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, WM-473, WM-369, 342, and WM-429.

- The method according to claim 15, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, and WM-120.
- The method according to claim 15, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290.
- (A) an adsorbent attached to a substrate that retains one or more of biomarkers A kit for detecting and diagnosing lung adenocarcinoma, comprising clected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-:90, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-
 - 310, WM-292, WM-120, WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, 70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, VM-340, WM-48, WM-389, WM-450, WM-47, WM-343, WM-17, WM-583, WM-WM-473, WM-369, WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WM-307, WM-278, WM-342, and WM-429, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- A kit according to claim 18, further comprising a washing solution or instructions for making a washing solution.
- A kit according to claim 18, wherein the substrate is a SBLDI probe that comprises functionalities that allow for cation exchange.
- 131, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, WM-290, subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-366, WM-65, WM-70, WM-341, WM-429, WM-347, WM-17, WM-47, WM-WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, A method for qualifying squamous cell lung carcinoma status in a

WM-420, WM-450, WM-369, WM-279, WM-342, WM-471, WM-674, WM-120, WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-138, WM-20, WM-287, WM-83, WM-154, and WM-128.

- The method according to claim 21, wherein the protein is selected from WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, and the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134,
- The method according to claim 21, wherein the protein is selected from the group consisting of WM-447, WM-61, WM-277, WM-446, and WM-133.
- 24. A method for qualifying status of squamous cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- recognition analysis that is keyed to at least one peak selected from either a first group WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, WM-70, WM-WM-279, WM-342, WM-471, WM-674, WM-120, WM-20, WM-287, WM-83, WMconsisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, 41, WM-429, WM-347, WM-17, WM-47, WM-431, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, WM-290, WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-138, WM-420, WM-450, WM-369, (B) extracting data from the spectrum and subjecting the data to pattern-154, and WM-128.
- The method according to claim 24, wherein the protein is selected from WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, and the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-70.
- The method according to claim 24, wherein the protein is selected from the group consisting of WM-41, WM-61, WM-277, WM-446, and WM-133.
- A kit for detecting and diagnosing squamous cell lung carcinoma, comprising

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biomarkers selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, WM-70, WM-341, WM-429, WM-347, WM-17, WM-47, WM-138, WM-420, WM-450, WM-369, WM-279, WM-342, WM-471, WM-674, WM-290, WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-431, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, (A) an adsorbent attached to a substrate that retains one or more of the WM-120, WM-20, WM-287, WM-83, WM-154, and WM-128, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- A kit according to claim 27, further comprising a washing solution or instructions for making a washing solution.
- A kit according to claim 27, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 51, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-339, WM-457, WM-86, WM-506, WM-72, WM-287, WM-82, WM-528, WM-A method for qualifying small cell lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-85, WM-73, WM-138, WM-384, WM-83, WM-450, WM-310, WM-277, WM-79, WM-65, WM-685, WM-473, WM-343, WM-466, WM-341, WM-340, WM-363, WM-207, WM-278, WM-290, WM-366, WM-472, WM-420, WM-147, WM-55, WM-669, WM-357, WM-429, and WM-279.
- The method according to claim 30, wherein the protein is selected from WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, and the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-685.
- The method according to claim 30, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, and WM-61.
- A method for qualifying status of small cell lung carcinoma in a subject, comprising

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(A) providing a spectrum generated by mass spectroscopic analysis of a

- biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-436, WM-646, WM-455, WM-65, WM-685, WM-446, WM-341, WM-340, WM-363, WM-363, WM-373, WM-86, WM-73, WM-86, WM-72, WM-87, WM-82, WM-528, WM-528, WM-73, WM-138, WM-364, WM-450, WM-420, WM-471, WM-420, WM-452, WM-450, WM-420, WM-429, WM-429, WM-472, WM-420, WM-147, WM-55, WM-669, WM-357, WM-429, and WM-279.
- 34. The method according to claim 33, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, and WM-685.
 - The method according to claim 33, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, and WM-61.
 - 36. A kit for detecting and diagnosing small cell lung carcinoma,
 - commisino
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-622, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, WM-65, WM-473, WM-86, WM-86, WM-86, WM-341, WM-341, WM-341, WM-343, WM-363, WM-37, WM-37, WM-86, WM-384, WM-86, WM-450, WM-470, WM-270, WM-296, WM-296, WM-472, WM-420, WM-147, WM-35, WM-669, WM-357, WM-429, and WM-279, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 37. A kit according to claim 36, further comprising a washing solution or instructions for making a washing solution.

- 38. A kit according to claim 36, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 39. A method for qualifying non-small cell hing carcinorns status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-485, WM-480, WM-283, WM-203, WM-207, WM-436, WM-382, WM-61, WM-167, WM-382, WM-285, WM-610, WM-383, WM-11, WM-265, WM-451, WM-419, WM-220, WM-6885, WM-338, WM-71, WM-266, WM-70, WM-845, WM-675, WM-446, WM-120, WM-267, WM-465, WM-1338, WM-1465, WM-153, and WM-38.
- The method according to claim 39, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-348, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, and WM-456.
- The method according to claim 39, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, and WM-340.
 - 42. A method for qualifying status of non-small cell lung carcinoms in a subject, comprising

 (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-439, WM-489, WM-669, WM-474, WM-652, WM-154, WM-587, WM-456, WM-480, WM-283, WM-281, WM-68, WM-382, WM-285, WM-680, WM-282, WM-686, WM-383, WM-429, WM-11, WM-208, WM-451, WM-473, WM-420, WM-421, WM-420, WM-455, WM-465, WM-485, WM-485, WM-343, WM-343, WM-15, and WM-345, WM-466, WM-446, WM-120, WM-267, WM-466, WM-347, WM-155, and WM-38.

- The method according to claim 42, wherein the protein is selected from WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, and the group consisting of WM-341, WM-342, WM-343, WM-48, WM-346, WM-456.
- The method according to claim 42, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, and WM-340.
- A kit for detecting and diagnosing non-small cell lung carcinoma, comprising
- MM-11, WM-208, WM-451, WM-473, WM-220, WM-685, WM-338, WM-71, WM-266, WM-70, WM-545, WM-675, WM-446, WM-120, WM-267, WM-466, WM-347, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, WM-456, WM-285, WM-650, WM-203, WM-119, WM-282, WM-686, WM-383, WM-429, biomarkers WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-450, WM-283, WM-207, WM-436, WM-384, WM-61, WM-167, WM-382, (A) an adsorbent attached to a substrate that retains one or more of the WM-153, and WM-38, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 46. A kit according to claim 45, further comprising a washing solution or instructions for making a washing solution.
- 47. A kit according to claim 45, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- comprised of analyzing a biological sample from said subject for a level of a protein 48. A method for qualifying large cell lung carcinoma status in a subject, :90, WM-328, WM-447, WM-684, WM-183, WM-190, WM-686, WM-397, WM-66, WM-20, WM-17, WM-545, WM-47, WM-191, WM-147, WM-480, WM-590, 547, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WMselected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-55, and WM-488.

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- The method according to claim 48, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, and WM-447.
- The method according to claim 48, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, and WM-647.
- A method for qualifying status of large cell lung carcinoms in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-345, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, (B) extracting data from the spectrum and subjecting the data to pattemrecognition analysis that is keyed to at least one peak selected from the group WM-55, and WM-488.
- The method according to claim 51, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, and WM-447.
- The method according to claim 51, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, and WM-647.
- A kit for detecting and diagnosing large cell lung carcinoma,
- WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, biomarkers WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, (A) an adsorbent attached to a substrate that retains one or more of the

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545, WM.47, WM.191, WM.147, WM.480, WM.590, WM.218, WM.655, WM.655, WM.651, WM.651, WM.366, WM.403, WM.418, WM.430, WM.456, WM.305, WM.307, WM.375, WM.131, WM.706, WM.398, WM.309, WM.587, WM.375, WM.131, WM.706, WM.398, WM.309, WM.55, and WM.488, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 55. A kit according to claim 50, further comprising a washing solution or instructions for making a washing solution.
- 56. A kit according to claim 50, wherein the substrate is a SELD! probe that comprises functionalities that allow for carion exchange.
- 57. A method for distinguishing hung adenocarcinoma from squamous lung carcinoma in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-62, WM-415, WM-185, WM-385, WM-385, WM-117, WM-347, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-64, WM-117, WM-211, WM-362, WM-313, WM-313, WM-414, WM-277, WM-141, WM-64, WM-115, WM-447, WM-383, WM-38, WM-63, WM-142, WM-85, WM-86, WM-85, WM-82), WM-276, WM-83, WM-85, WM-85, WM-82, WM-17, WM-203, WM-83, WM-412, WM-96, WM-74, WM-457, WM-412, WM-96, WM-74, WM-49, and WM-49.
- 58. The method according to claim 57, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, and WM-211.
- The method according to claim 57, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, and WM-347.
- A method for distinguishing lung adenocarcinoma from squamous lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from the group

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consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-999, WM-1211, WM-289, WM-363, WM-61, WM-117, WM-211, WM-362, WM-133, WM-414, WM-277, WM-141, WM-64, WM-135, WM-447, WM-383, WM-338, WM-63, WM-142, WM-446, WM-186, WM-111, WM-445, WM-455, WM-276, WM-444, WM-181, WM-35, WM-285, WM-486, WM-81, WM-82, WM-81, WM-496, WM-457, WM-431, WM-340, and WM-49.

- The method according to claim 60, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, and WM-211.
- The method according to claim 60, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, and WM-347.
- A kit for distinguishing lung adenocarcinoma from squamous lung carcinoma, comprising

(A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-621, WM-648, WM-657, WM-290, WM-328, WM-447, WM-684, WM-199, WM-686, WM-397, WM-466, WM-20, WM-17, WM-545, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-706, WM-398, WM-309, WM-55, and WM-488, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 64. A kit according to claim 63, further comprising a washing solution or instructions for making a washing solution.
 - 65. A kit according to claim 63, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 66. A method for distinguishing lung adenocarcinoma from small cell lung carcinoma in a subject, comprised of analyzing a biological sample from said subject

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for a level of a protein selected from the group consisting of WM-457, WM-72, WM-369, WM-79, WM-72, WM-64, WM-320, WM-419, WM-82, WM-82, WM-412, WM-440, WM-455, WM-313, WM-456, WM-86, WM-70, WM-246, WM-312, WM-412, WM-418, WM-83, WM-257, WM-138, WM-47, WM-252, WM-282, WM-60, WM-68, WM-325, WM-402, WM-411, WM-405, WM-75, WM-417, WM-387, WM-26, WM-410, WM-420, WM-164, WM-67, WM-66, WM-391, WM-340, WM-428, WM-182.

- 67. The method according to claim 66, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-82, WM-53, WM-412, WM-440, and WM-455.
- The method according to claim 66, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, and WM-79.
- 69. A method for distinguishing lung adenocarcinoma from small cell lung carcinoma in a subject, comprising
 - (A) providing a spectrum generated by mass spectroscopic analysis of a

biological sample taken from the subject, and

- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-313, WM-419, WM-85, WM-82, WM-360, WM-12, WM-440, WM-455, WM-313, WM-456, WM-138, WM-70, WM-246, WM-60, WM-60, WM-68, WM-325, WM-402, WM-411, WM-405, WM-75, WM-417, WM-387, WM-26, WM-410, WM-402, WM-411, WM-405, WM-51, WM-321, WM-321, WM-331, WM-
- 70. The method according to claim 69, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-83, WM-412, WM-440, and WM-A65.

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 The method according to claim 69, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79.

72. A kit for distinguishing bung adenocarcinoma from small cell lung carcinoma, comprising

(A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-466, WM-466, WM-486, WM-355, WM-447, WM-133, WM-245, WM-52, WM-96, WM-238, WM-243, WM-138, WM-247, WM-134, WM-240, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-242, WM-556, WM-63, WM-239, WM-234, WM-274, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37, and

(B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.

73. A kit according to claim 72, further comprising a washing solution or instructions for making a washing solution.

74. A kit according to claim 72, wherein the substrate is a SELDI probe that

74. A ket according to claim 72, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.

- 75. A mothod for distinguishing squamous cell hung carcinoma from small cell lung carcinoma in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-276, WM-277, WM-362, WM-263, WM-363, WM-347, WM-53, WM-254, WM-177, WM-252, WM-431, WM-466, WM-365, WM-477, WM-133, WM-248, WM-246, WM-586, WM-134, WM-248, WM-247, WM-187, WM-242, WM-240, WM-256, WM-256, WM-203, WM-2111, WM-96, WM-247, WM-187, WM-242, WM-256, WM-63, WM-239, WM-234, WM-274, WM-270, WM-310, WM-336, WM-336, WM-371, WM-237, WM-261, WM-237, WM-237, WM-288, WM-3384, and WM-37.
- The method according to claim 75, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-357, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, and WM-447

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77. The method according to claim 75, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, and WM-363.

- 78. A method for distinguishing squamous cell lung carcinoma from small cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-354, WM-17, WM-254, WM-431, WM-431, WM-481, WM-481, WM-481, WM-481, WM-481, WM-482, WM-528, WM-138, WM-138, WM-62, WM-580, WM-134, WM-240, WM-256, WM-239, WM-111, WM-95, WM-247, WM-157, WM-242, WM-56, WM-63, WM-67, WM-234, WM-274, WM-285, WM-288, WM-384, and WM-37.
- 79. The method according to claim 78, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, and WM-447.
- The method according to claim 78, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, and WM-363.
- A kit for distinguishing squamous cell hung carcinoma from small cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-276, WM-377, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, WM-447, WM-133, WM-248, WM-52, WM-96, WM-238, WM-243, WM-134, WM-246, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-556, WM-63, WM-234, WM-234, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37, and

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(B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.

- 82. A kit according to claim 81, further comprising a washing solution or instructions for making a washing solution.
- 83. A kit according to claim 81, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 84. Software for qualifying lung carcinoma status in a subject, comprising an algorithm for analyzing data extracted from a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, wherein said data relates to one or more biomarkers selected from either a first group consisting of
- (i) IM-522, IM-573, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-337, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-166, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-560, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, IM-168, IM-568,

or from a second group consisting of

- (ii) WM-61, WM-47, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-438, WM-477, WM-420, WM-292, WM-431, WM-455, WM-360, WM-384, WM-384, WM-389, WM-63, WM-63, WM-384, WM-360, WM-138, WM-138, WM-138, WM-138, WM-138, WM-130.
- 85. Software according to claim 84, wherein said algorithm carries out a pattern-recognition analysis that is keyed to data relating to at least one of the biomarkers.
- 86. Software according to claim 85, wherein said algorithm comprises classification tree analysis that is keyed to data relating to at least one of the biomarkers.

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- artificial neural network analysis that is keyed to data relating to at least one of the Software according to claim 85, wherein said algorithm comprises 87. biomarkers.
- A method for qualifying lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a diagnostic level of a biomarker that is serun amyloid A protein or a fragment thereof.
- A method according to claim 88, wherein said serum biomarker has an apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Daltons.
 - A method according to claim 89, wherein said serum biomarker has an apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, 7941, 8152, 8952, or 10851 Daltons:
- A method according to claim 88, wherein said serum biomarker has an apparent molecular weight of about 11.5 to 11.7 kD.
- 92. A method according to claim 88, for qualifying risk of lung adenocarcinoma.
- A method according to claim 88, for qualifying risk of squamous cell lung carcinoma.
- A method according to claim 88, for qualifying risk of small cell lung carcinoma.
- A method according to claim 88, for qualifying risk of non-small cell lung carcinoma.
- A method according to claim 88, for qualifying risk of large cell lung carcinoma.
- (A) an adsorbent attached to a substrate that retains one or more of the A kit for detecting and diagnosing hing carcinoma, comprising biomarkers that are serum amyloid A protein or a fragment theseof. ۶.

(B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.

- apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, A kit according to claim 97, wherein said serum biomarker has an 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Daltons.
- apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, A kit according to claim 98, wherein said serum biomarker has an 7941, 8152, 8952, or 10851 Daltons.
- 100. A kit according to claim 97, wherein said serum biomarker has an apparent molecular weight of about 11.5 to 11.7 kD.
- 101. A kit according to claim 97, further comprising a washing solution or instructions for making a washing solution.
- 102. A kit according to claim 97, wherein the substrate is a SELDI probe.

FIGURE 1A

								•				
MARKER ID	WM	FRACTION	MARKER ID	WW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	£
IM-1	2011	. А	IM-37	3893	A	IM-72	54026	A	IM-109	2882	. B	WO 2001/061410
IM-2	2030	A	IM-38	3960	A	IM-73	60170	A	IM-110	2967	В.	20
IM-3	2069	A	IM-39	3972	A	IM-75	74372	Α	IM-111	2977	B	Ę
DM-4	2128	Α	IM-40	3984	A	IM-76	75545	, A	. iM-112	2994	В	累
IM-5	2146	A	IM-41 .	4088	Α	IM-77	77543	A	DM-113	3031	В	=
IM-6	2186	A	IM-42	4178	Α.	IM-78	79507	A	IM-114	3048	В.	•
IM-7	2232	Α	IM-43	4287	Α	IM-79	B9854	A	IM-115	3148	8	
IM-8	2277	A	IM-44	4297	A	IM-80	101831	Α	IM-116	3166	В	•
IM-9	2295	Α	IM-45	4309	A	IM-81	104301	Α	IM-117	3283	В	
IM-10	2318	Α	IM-46	4484	Α	IM-82	125160	, A .	IM-118	3308	8	
IM-11	. 2411	A	IM-47	4649	A	IM-83 .	132976	A	BM-119	3332	В	
IM-12	2434	A	IM-48	4798	Α	IM-84	149099	Α.	IM-120	3432	В	•
IM-13	2467	' A	IM-49	5104	A	IM-85	2016	В	IM-121	3450	. 8	
IM-14	2482	. A	IM-50	5918	Α	IM-86	2029	В	IM-122	3561	В	
IM-16	2498	A	IM-51	6122	Α.	IM-87	2144	В	IM-123	3615	В	
IM-18	2565	Α .	IM-52	6192	. А	IM-88	2130	В	IM-124	3714		
IM-17	2574	Α.	IM-53	6452	Α .	IM-89	2168		IM-125	3730		1/46
IM-18	2586	. A	IM-54	6660	Α	IM-80	2184		IM-126	3834		•
IM-19	2605	. A	IM-55	7768	Α	IM-91	2200		IM-127	3899	B	
IM-20	2722	Α .	IM-56	8145	A	IM-92	2284	. 8	IM-128	3969		
IM-21	2746	Α.	DA-57	8954	Α	IM-93	2289	В	IM-129	3986		
IM-22	2788	. A	IM-58	9312	Α	IM-04	2314		IM-130	3997		
IM-23	2855	Α .	IM-59	9449	, А	IM-95	2414		IM-131	4013		
IM-24	2871	Α	IM-60	70272	A	IM-98	2428	8.	IM-132	4181		
IM-25	2984	A	RA-61	11683	. A	IM-97	2451		IM-133	4297		•
IM-26	3030	. A	IM-62	13376	A	IM-98	2468	В	IM-134	4311	В	
DM-27	3144	Α .	IM-63	14698	. А	IM-89	2483		IM-135	. 4465		
W-28	3243	Α .	IM-84	15190	Α	IM-100	2565		IM-136	4484		7
IM-29	3273	Α'	IM-64	66758	A	IM-101 ·	2583	В	. IM-137	4579		3
IM-30	3290	1 A	IM-65	15951	Α	IM-102	2597		IM-138	4508		. 3
IM-31	3369		IM-66	15172		LM-103	2697		IM-139	4669		, S
IM-32	3445		IM-67	15925	Α.	IM-104	2715		IM-140	4747		` <u>E</u>
IM-33	3483		IM-68	23436	. А	IM-105	2740		IM-141	4882		2
IM-34	3676		IM-69	39794	Α	IM-106	2752	. В	IM-142	4891		PCT/US2003/037090
IM-35	3779		IM-70	44166	A	IM-107	2767		IM-143	5033		8
IM-36	3793	Α.	IM-71	48890	A	IM-108	2865	В	184-144	5077	₽ 6	
			•			• •			•			

FIGURE 1B

						•				MW	FRACTION		·
MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID IM-253	3733	C		
IM-145	5099	В	DM-181	16018	В	IM-217	2130	c		3833	č		
IM-146	5143	В	IM-182	17346	В	(M-218	2145	C	IM-254	3900	č	c	1
IM-147	5158	8	IM-183	18311	В	IM-219	2167	C	IM-255	4010	č	c	
IM-148	5272	В	IM-184	22586	В	IM-220	2182		IM-258	4145	č		
IM-149	5306	В	IM-185	23422	В	1M-221	2199		IM-257	4187	č		:
IM-150	5349	В	1M-188	27969	8	IM-222	2211	C	IM-258	4299	č		
IM-151	5364	В	IM-187	33283	8	IM-223	2230		IM-259	4289 4488			
IM-152	5421	B	IM-188	39808	8	IM-224	2250		IM-260				
IM-153	5554	В	DM-189	43110	B	IM-225	2280		IM-261	4582 4813			
IM-154	5711	В	IM-190	44454	8	IM-226 .	2297		IM-262				
IM-155	5876		IM-191	47215	В	IM-227	2317		IM-263	4876			
IM-156	5916		IM-192	53784		IM-228	2412		IM-264	5032			
· IM-167	5931	8	IM-193	55952	В	IM-229	2428		IM-265	5347			
IM-158	5988		IM-194	60573		IM-230	2468		IM-268	5365			
IM-158 IM-159	6137		IM-195	66346		IM-231	2481		IM-287	5932			
IM-160	6200		IM-196	73387		IM-232	2498		1M-268	7767			
	6443		BA-197	79203		IM-233	2567		IM-269	7973			2
IM-161	6844		DM-198	89302		6M-234	2585		IM-270	8143			7,4
IM-162	6958		DM-199	94226		IM-235	2599		IM-271	9187			
IM-163	7481		IM-200	99358		IM-236	2698	3 C	IM-272	9293			
IM-164			IM-201	102090		IM-237	2719	5 C	IM-273	1170			
IM-165	7568		IM-202	107199		IM-238	274	5 C	[M-274	14041			
IM-166	7765		IM-203	116936		IM-239	276	. С	IM-275	15114			
IM-167	7955		IM-203	119487		IM-240	286	7. C	IM-276	15931			
IM-168	8144		IM-206	12210		IM-241	288	s C	IM-277	2232			
IM-169	8698		IM-206	12543		IM-242	299		IM-278	2800			
IM-170	8821			13205		IM-243	305		IM-279	3329			
IM-171	8944		IM-207	13851		IM-244	309		DM-280	3977			
BM-172	9136		IM-208			IM-245	315		IM-281	4448			
IM-173	9298		IM-209	14514		IM-246	316		IM-282	4730			
IM-174	9390		IM-210			IM-247	328		IM-283	-5062	5 C		
IM-175	9516		IM-211	16857		IM-248	330		IM-284	5589	8 C		
IM-178	1171		IM-212	17339		IM-249	333		M-285	6088	2 C -		
IM-177	11914		IM-213 .	201			344		IM-286	6629			
IM-178	14033		IM-214	203		IM-250	361		IM-287	7889			
IM-179	15110		IM-215	205		IM-251			(M-288	8384			,
IM-180	1583	3 B	IM-216	209	6 C	IM-252	370	9 C	1147-200	5554			

MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	
IM-289	89081	С	tM-325	2565	D	IM-381	13857	D	IM-397	2082	Ė	•
IM-290	94147	C	IM-326	2582	oʻ	IM-362	14058	D ·	IM-398	2128	E	WO 2004/061410
IM-291	99324	C	IM-327	2597	D	IM-383	15108	D	IM-399	2148	E	20
IM-292	107183	C	DM-328	2716	D	(M-364	15844	· D	IM-400	2170	E	Ę
IM-293	110350	C	DM-329	2747	D	IM-365	22243	D	IM-401	2187	E	36
IM-294	113339	. с	IM-330	- 2767	D	tM-368	25465	D	1M-402	2206	€ .	
IM-295	118291	С	IM-331	2866	D	IM-367	28022	D	IM-403	2232	Ε	5
IM-298	122769	C	IM-332	2882	Ð.	IM-368	33272	Ð	IM-404	2250	E	
IM-297	131908	C	IM-333	2994	D	IM-369	40149	D	IM-405	2279	E	
IM-298	145248	C	IM-334	3032	· D	IM-370	43113	. D .	IM-408	2296	E	
IM-299	159252	C	IM-335 -	3050	D	IM-371	44219	D .	IM-407	2314	E	
IM-300	165164	C	IM-336	314B	D	IM-372	47196	D.	1M-408	2354	£	,
IM-301	174928	C	IM-337	3164	D.	IM-373	51062	D	IM-409	2394	E	
IM-302	196003	C	IM-338	3278	D	IM-374	56082	D .	IM-410	2413	E	
IM-303	2007	D	IM-339	3334	D .	IM-375	58239	D	· IM-411	2438	E	
IM-304	2016	D	IM-340	3385	Đ	*IM-376	60285	D ·	IM-412	2457	E	
IM-305	2030	D	IM-341	3432	Đ	IM-377	66148	D	IM-418	2466		
DM-306	2052	D	IM-342	3451	D.	DM-378	73668	D	IM-414	2489	E	34/6
IM-307	2099	D	IM-343	3817	D.	IM-379	77433	D	IM-415	2568	Ę	₹.
IM-308	2130	D	IN-344	3701	D ·	IM-380	79985	Þ	IM-416	2583	E	
IM-309	2144	D	IM-345	3725	D	IM-381	60844		IM-417	2612	E	
IM-310	2154	D	IM-346	3833	D	IM-382 .	88962	Ð	IM-418	2662	E ·	
IM-311	2166	. D	IM-347	3899	D	IM-383	94399	D	IM-419	2723	€ '	
IM-312	2184	D	IM-348	4008	D	IM-384	99419	D	IM-420	2738	E	
IM-313	2204	D	IM-349	4157	, D	IM-385	108395	Ď	IM-421	2750	E E	
IM-314	2231	D	IM-350	4297	D	tM-386	116433	٥	IM-422	2849	E	
IM-315	2252	ם .	IM-351	4580	D	IM-387	123337	D	IM-423	2867		•
IM-316	2275	D	IM-352	4805	D	IM-388	131977	۵	'IM-424	3036	E	
IM-317	2299	.D	IM-353	6946	D	IM-389	145658	D	PM-425	3147	E	7
IM-318	2316	D	IM-354	7053	D	IM-390	152603	Ď	IM-426	3281	E	PCT/US2003/037090
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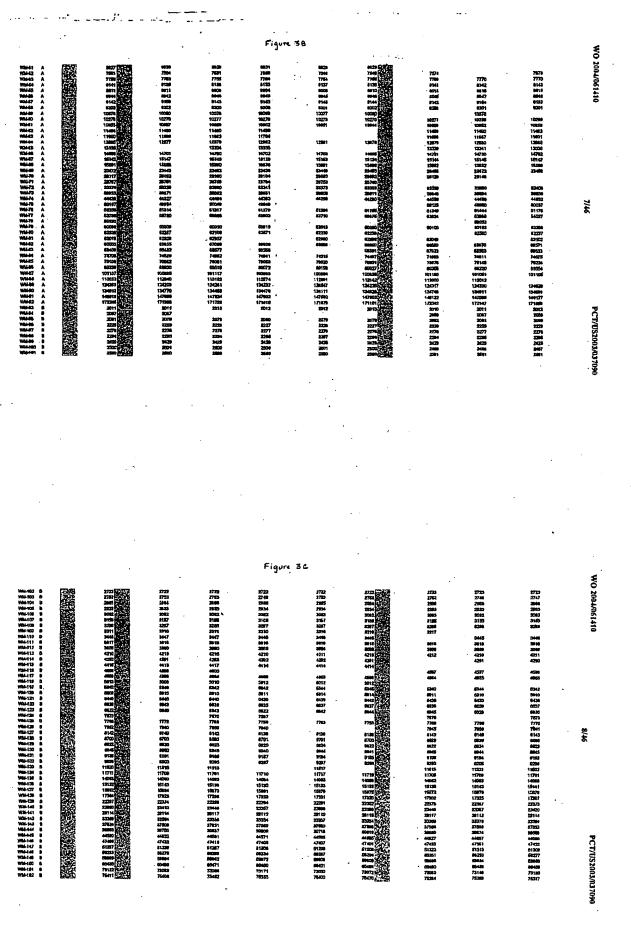
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FIGURE	10

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IM-435	4257		IM-471	100270	E	IM-507	4473	F	IM-543	116889	F
IM-438	4277	E	IM-472	109638	E	IM-508	4631	F	IM-544	132711	F
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IM-438	4369	E	IM-474	132843		IM-510	5862	F	IM-546	160768	F
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IM-440 ·	4488		IM-476	152199		IM-512	6941	F			
IM-441	4541		IM-477	188481	E	IM-513	7626	f			
IM-442	4834		IM-478	176835		IM-514	7772	F			
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IM-444	5862		IM-480	2030		IM-516	B150	F	•		
IM-445	5911		IM-481	2128		IM-517	8954	F			
IM-446	8849		IM-482	2149		IM-518	9300	F			
IM-447	6952		IM-483	2188		IM-519	11545			•	
IM-448	7769	E	IM-484	2207		IM-520	11717	F			
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IM-454	11721		IM-480	2467		IM-526	23135				
IM-455	13910		IM-491	2485		IM-527	28135				
IM-456	15919		IM-482	2582		IM-528	33577				
IM-457	22422		IM-493	2605		IM-529	39813				
IM-458	28233		IM-494	2697		IM-630	42344	F			
IM-459	33490		IM-495	2751		IM-531	43274	F			
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IM-483	50954		IM-499	3372		IM-535	50079				
IM-464	54478		1M-500	3440		IM-538	66690				
LM-465	60041		IM-501	3488		IM-537	75122				
IM-466	66852		IM-502	3717		IM-538	78429				
IM-467	75580		IM-503	3890		IM-539	81249	F	•		
1M-468	79463	E	IM-504	4155	F-	IM-540	89384	F			

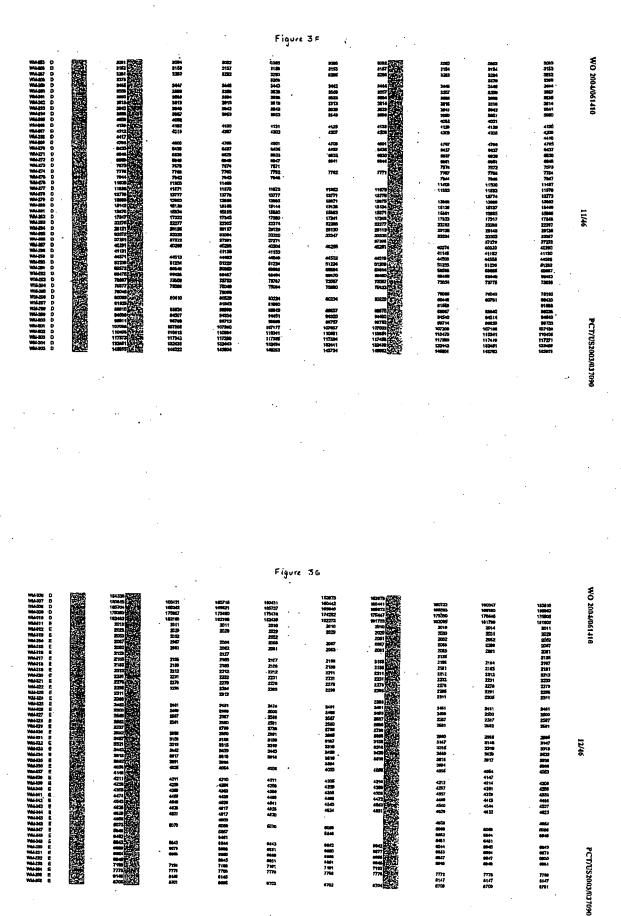
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26 27 28 29 30 31 32 33 34 35 36 37	2752 13910 5662 5988 5347 5918 6137 5916 4470 5931 4631 7772 176635	IM-106 IM-455 IM-450 IM-265 IM-50 IM-159 IM-159 IM-159 IM-157 IM-508 IM-514 IM-478						PCT/US2003/037096

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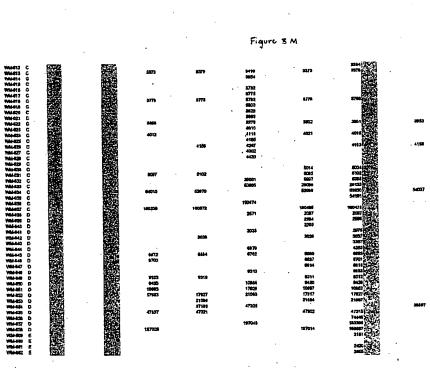


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tank	Normal vs Cancer	Adeno ve Norssal	Squamous vs Hornad	Small Cell ve Hormal	Non-email Call va Homad	Large Coll vs Normal	Adena va Squamous	Adeno vs Sizzali Çali	Squamous vs Small Cell
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ł	- WNJ-447	WN4-652	WOA-61	WN4-706	WM-342	W94-26	WM-415	WM472	WM-277 -
1	WOA-446	WM-81 .	V0A-277	WM-329	WA-343	W34-400	WA-152	W94-289	VRA-302
1	WN-133	WW-448	1004-465	W16-467	T04-48	WM-134	W04-365	W04-78	WM-257
	W04-119	WM-290	W0A-133	V04-01	WM-340	WM-647	. WM-347	W04-79	WM-363 .
1	W34-278	WM-353	W34-134	WALEST	WA-348	WM-277	WILLIA	WM-73	WM-363 -
,	W34-134	WM-133	WAA-803	W04-202	WM-47	WM-310	WEAS	W04-64	WM-53
:	W34-363	WM-341	W04-302	WBA-462	WAA330 .	W34-363	W64-108	W04-329	WM-254
1	WN-282	WN-205	WAA-276	W04-656	W04-380	WM-448	WALCO	W04-419	WM-254 WM-17
0	W34-802	W04-358	W0A-708	W94-134	704-669	WM-221	WA-151	WM-8S	WM-17
H	W94-120	WM-282	W64-203	WM-203	WM-447	WMAGAR	WA4-260	W94-82	W04431
2	W54-290	W04-362	W64-400	W04648	W04-852	WH-857	WM-3ES	W84-63	W84613
9	WN-65	W34-810	WAA300	W94-458	WM-104	WM-290	WALET	WM412	WH-446
u	WAI-277	WN-202	WAA-65	WMACS	WM-587	WM-328		700-440	W34-355
15	WM-TO	WN4-120	WOATO	WAAGM	WM-455	WMAST	WM-211	WM-455	Wh4-447
15	W74-363	WW-134	WA4-361	WM-673	WM-430	WM-634		WM-313	W04-133
7	WM-17	WN-276	WILLED	V94-342	Y04-253	WM-183 .	WM-130	WM-456	W04-245
	WM-473	WN4-428	WAA-347	VILCES		WM-190	· WM-414	WM-CSE WM-SSE	WM-52
9		W94-277	WAA-17	W34361	WM-436	WM-686	W04-277	W21-70	WILLIAM
0	MM-503	W7N-20	WQA-47	WMASKE	WM-384	WM-397	WM-141	WM-248	W14-236
7	WW-270	WM-119	WAA-631	WR4-353	V6461	WM-406	WN4-04	W04-860	W94-243
2	WM-279	WM-340	WH-62	W84-328	WM-167	WM-20	WM-133	WM-180	V04-136
•	WH-61	V/M-48	WIA-473	VM-457	W04-3002	WW-17	W04-447	WM-418	VIA-62
•	WM-358	WN4-339	W04.534	WM-86	WM-285	WM-545	WMARE	WM-83	WM-580
•	WM-488	WM-450	WM-436	W94-508	WALESD	WM-67	WM4-336	WN-257	W14-134
5	W34-425	V04-47	WALKER	WM-72	984-203	WM-191	WM4-63	MJM-128	W16-24D
7	WM-364	W94343	W04-282	WM-267	WM-119	WM-147	WM-142	WM-47	WM-258
2	WM-257	WN-17	W04.350	W14-82	WM-262	W14-480	W14-446	WM-252	WM-200
9	WM-620	WM-523	W04-290	W04-528	WM-686	WM-500	W04-186	WM-282	W54111
	WM-892	WM-70	WM4-270	WINAS	WM-383	WM-218	WM-111	WALGO	WALOS
4	W14-431	WM-708	WALLED	W04-73	WM-429	WM-285	WM-445	WALES	WA4-247
2.	WM-453	Wh4348	WM-673	W04-536	W04-11	WM-622	WM-455	WA4-329 ·	VM-417 VM-157
•	WU-20	WM-4CB	WA4-345	WM-384	WM-206	WM-051	W04-276	WN-402	WM-342
4	WW-340	WN-648	WAASS	WALES	Whi-451	W34-300		WM-411	VM4-555
5	WM-19	WNL384	VM-485	WMA-4ED	WM-473	W14-403		WN-411	WM4655
₩.	WM-389	WM-335	WAA-645	WA-310	WM-220	WM-418		WAL-75	VINA-239
7	WAI-63	WM-294	WSA-138	W84-277	WM-685	WM-630		WM-75 WM-417	WM-234
•	WM-436	WM-339	WM-420	W64-79	WM-338	WM-465		WAI-867	WM-274
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29 40 41 42 43 44	Wu-450 Wu-468 Wu-343 Wu-343 Wu-341 Wu-339	WN-473 WN-329 WN-33 WN-223 WN-625 WIL-88	WA-450 WA-359 WA-279 WA-342 WA-479 WA-674	WM-207 WM-278 WM-280 WM-285 WM-472 WM-420	W1471 W14285 W1470 W14545 W14575 W14448	V96-714 V96-046 V96-189 V96-302 V96-567 V06-578	WM-39 WM-42 WM-17 WM-203 WM-412	WA425 WA410_ WA420 WA416 WA467 WA665	WM-370 WM-301 WM-409 WM-74 WM-201 WM-467
45 44 47 48 49 50	Wal-88 Wal-88 Wal-38 Wal-138 Wal-310	WM-25 WM-250 WM-278 WM-342 WM-429	WM-120 VM-20 WM-267 WM-83 WM-154 WM-128	WM-147 WM-66 WM-680 WM-167 WM-429 WM-278	WM-120 WM-267 WM-468 WM-347 WM-163 WM-38	W14-131 W14-706 W14-328 W14-329 W14-65 W14-486	WM-95 WM-74 WM-457 WM-431 WM-340 WM-49	WM-391 WM-340 WM-428 WM-188 WM-312 WM-152	WM-207 WM-262 WM-295 8/M-295 WM-304 WM-37

3897 7941 SAA 64-98 (3897.2) SAA 18-88 (7939.5) 4300 8152 SAA 54-93 (4302.5) SAA 25-98 (8150) 4490 8952 SAA 53-93 (4489) SAA 6-85 (8950) 4655 9233 SAA 5-44 (4655.0) SAA 16-97 (9235)

Figure 5

SAA 5-102 (10853.7)

10851

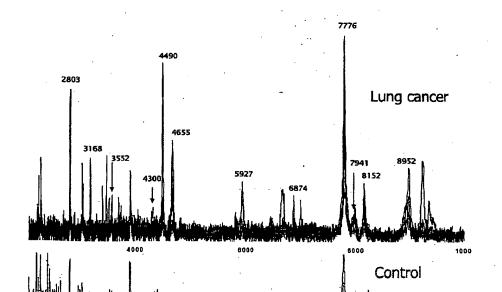
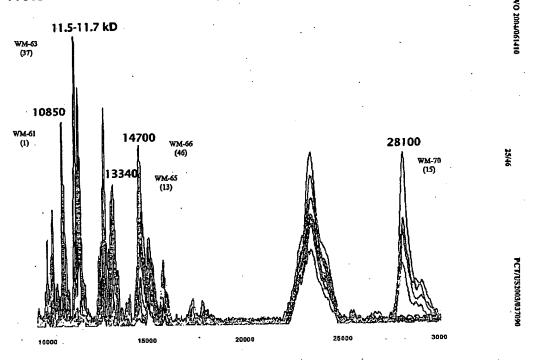
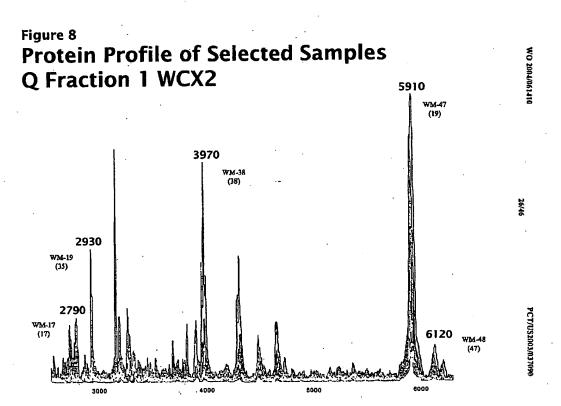


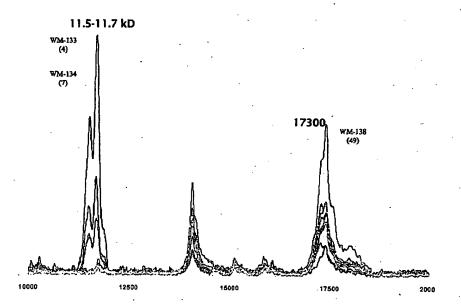
Figure 6

FIGURE 7
Protein Profile of Selected Samples Q Fraction 1 WCX2





Protein Profile of Selected Samples Q Fraction 2 WCX2



Protein Profile of Selected Samples Q Fraction 2 WCX2

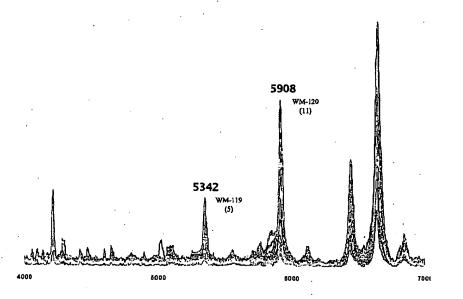


Figure 11 Protein Profile of Selected Samples Q Fraction 4 WCX2

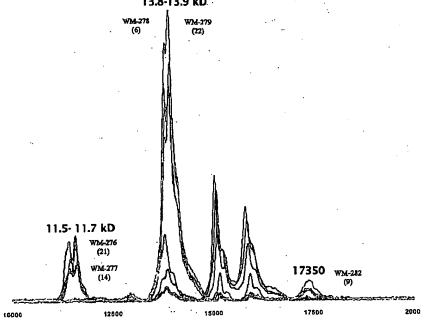
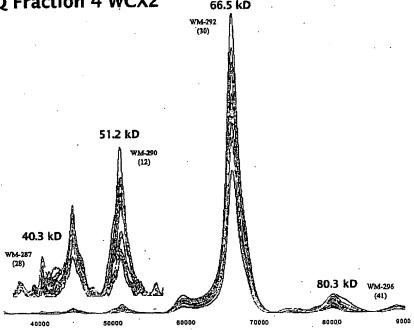
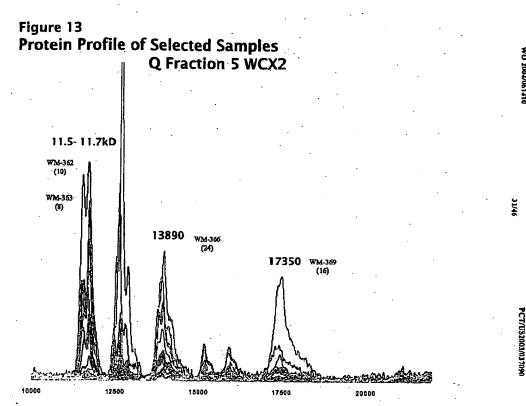


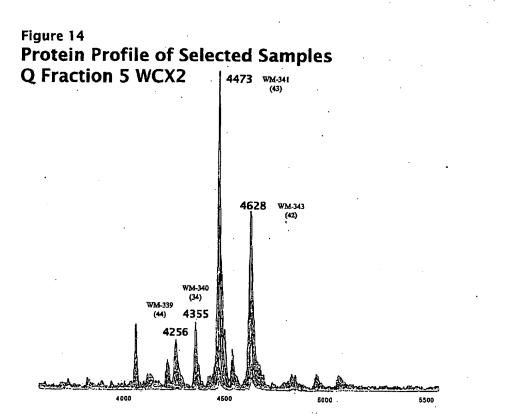
Figure 12
Protein Profile of Selected Samples
Q Fraction 4 WCX2
66.5 kD



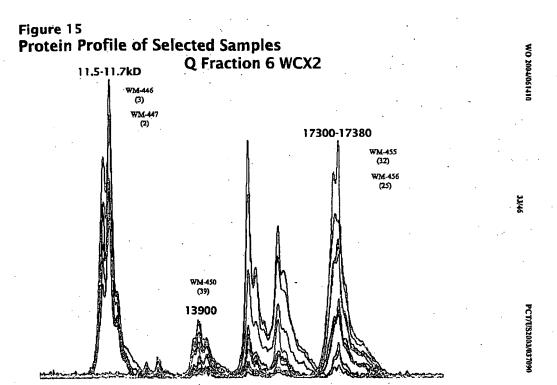
30/46

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32/46



Protein Profile of Selected Samples Q Fraction 6 WCX2

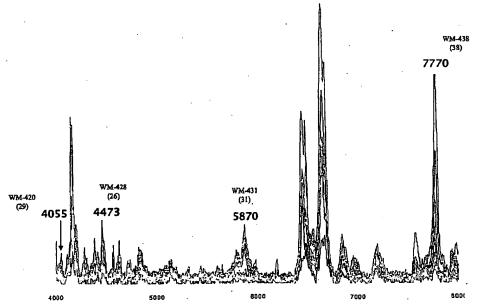
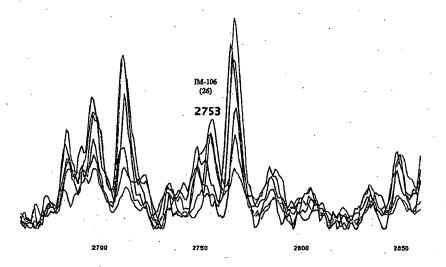


Figure 17.

Protein Profile of Selected Samples Q Fraction 2 IMAC-Cu(II)



Protein Profile of Selected Samples Q Fraction 2 IMAC-Cu(II)

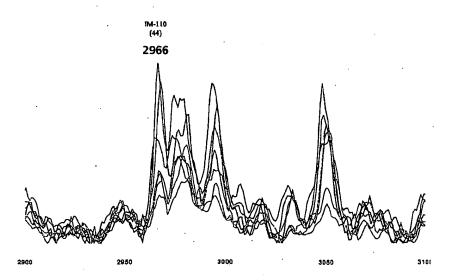
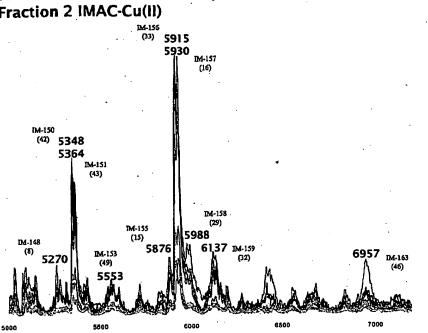
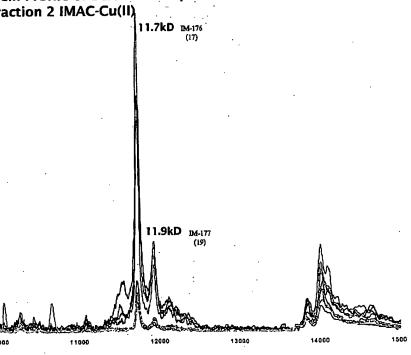
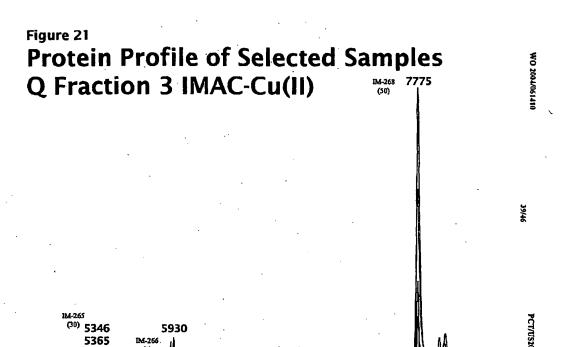


Figure 19
Protein Profile of Selected Samples
Q Fraction 2 IMAC-Cu(II)









Protein Profile of Selected Samples Q Fraction 3 IMAC-Cu(II)

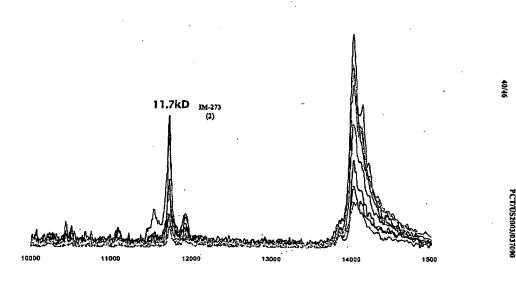


Figure 23
Protein Profile of Selected Samples
Q Fraction 5 IMAC-Cu(II)

M439 4470
(24) 4480 m.440
(20)

1M435 4276 4370
(25)

1M435 4276 4370
(27)

1M444 5860 5910 m.445
(18)

Protein Profile of Selected Samples Q Fraction 5 IMAC-Cu(II)

4000

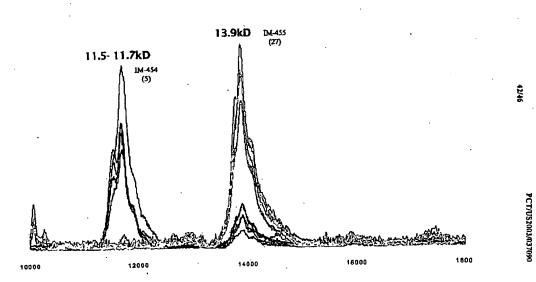


Figure 25
Protein Profile of Selected Samples
Q Fraction 5 IMAC-Cu(II)

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Protein Profile of Selected Samples Q Fraction 6 IMAC-Cu(II)

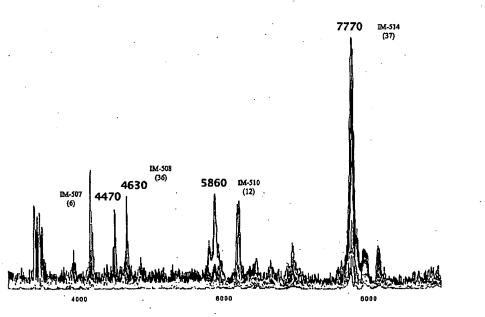


Figure 27
Protein Profile of Selected Samples
Q Fraction 6 IMAC-Cu(II)

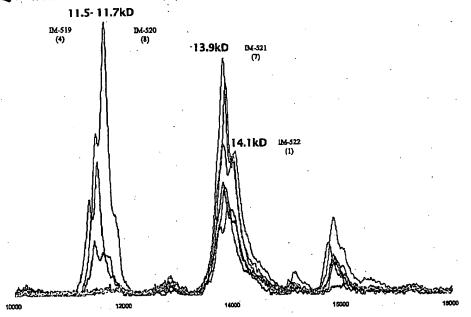
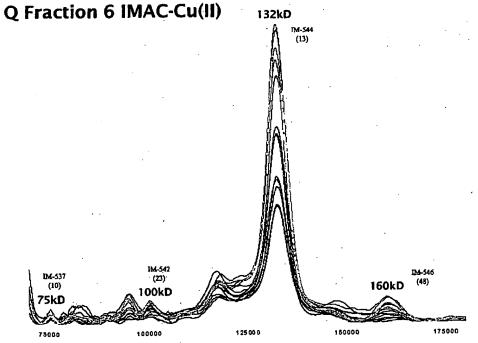


Figure 28
Protein Profile of Selected Samples
O Fraction 6 IMAC-Cu(II)
132kD



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